

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
- (ii) TITLE OF INVENTION: Novel Telomerase
- (iii) NUMBER OF SEQUENCES: 225
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESS: Townsend and Townsend and Crew LLP
 - (B) STREET: Two Embarcadero Center, 8th Floor
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: United States of America
 - (F) ZIP: 94111
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/854,050
 - (B) FILING DATE: 09-MAY-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/851,843
 - (B) FILING DATE: 06-MAY-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/846,017
 - (B) FILING DATE: 25-APR-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/844,419
 - (B) FILING DATE: 18-APR-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/724,643
 - (B) FILING DATE: 01-OCT-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Apple, Randolph T.
 - (B) REGISTRATION NUMBER: 36,429
 - (C) REFERENCE/DOCKET NUMBER: 015389-002930US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 576-0200

(B) TELEFAX: (415) 576-0300

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAACCCCAA AACCCCAAAA CCCCTTTT TAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA 60
TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA 120
TCAAGCTGAT AATCATGGCA TTCCTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC 180
TAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA 240
TTATAAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTAATCCACG 300
AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT 360
AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT TCATCAAGCG ATGTTTCAGA 420
TAGACAAAAA CTTCAATGAT TTGGATTTC AACTTAAGGA AATCAATTAG CAAAGACCCA 480
TTTATTAACA GCTCTTTCAA CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT 540
TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA 600
GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA 660
AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG 720
ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT 780
CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT 840
TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT 900
AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA 960
GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT 1020
TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGAACCGGAA 1080
ACAAAAAATC GAAAACCTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA 1140
GCTGTTTAGC TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA 1200
CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC AAAAGAAAGT 1260
TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTCAC AAAAACTTAT TGCTTGAGAA 1320
GATCAATACA AGAGAAATAT CATGGATGCA GGTGAGACC TCTGCAAAGC ATTTTTATTA 1380
TTTGTATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT 1440

CGTCGTCTCG CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA	1500
AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT	1560
AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT	1620
TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT	1680
GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC	1740
GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC	1800
TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTG	1860
CAAATGGAAG CAAGTTGGAC AACCAAACT CTTCTTTGCA ACTATGGATA TCGAAAAGTG	1920
ATATGATAGT GTAAACAGAG AAAAATATC AACATTCCTA AAAACTACTA AATTACTTTC	1980
TTCAGATTTT TGGATTATGA CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA	2040
TTCGAAAAAC TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT	2100
TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG AACAAAATGA	2160
CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA AGAAATTATT TTAAGAAAGA	2220
TAACCTACTT CAACCAGTCA TTAATATTTG CCAATATAAT TACATTAACT TTAATGGGAA	2280
GTTTTATAAA CAAACAAAAG GAATTCCTCA AGGTCTTGA GTTTCATCAA TTTTGTGATC	2340
ATTTTATTAT GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA	2400
CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC TTTTGATTAC	2460
AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAACTT ATAAACGTAA GTCGTGAAAA	2520
TGGATTTAAA TTCAATATGA AGAACTACA GACTAGTTTT CCATTAAGTC CAAGCAAATT	2580
TGCAAAATAC GGAATGGATA GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG	2640
GATTGGCATC TCAATTGATA TGAAAACCTC TGCTTTAATG CCAAATATTA ACTTGAGAAT	2700
AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT CAATGTGGCT	2760
CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC CATTATTTTA GAAAGACGAT	2820
TACAACCGAA GACTTTGCGA ATAAAACCTC CAACAAGTTA TTTATATCAG GCGGTTACAA	2880
ATACATGCAA TGAGCCAAAG AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG	2940
TATGATCGAC TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA	3000
CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG ACTTTTTCCT	3060
TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA AAGTACATTT TCAACAGAGT	3120
TTGCATGATC CTCAAGGCAA AAGAAGCAAA GCTAAAAAGT GACCAATGTC AATCTCTAAT	3180
TCAATATGAT GCATAGTCGA CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTTG	3240
TCTTATATAC TGGGGTTTTG GGGTTTTGGG GTTTTGGGG	3279

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
1 5 10 15
Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
20 25 30
Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
35 40 45
Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
50 55 60
Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
65 70 75 80
Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
85 90 95
Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
100 105 110
Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
115 120 125
Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
130 135 140
Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
145 150 155 160
Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
165 170 175
Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
180 185 190
Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
195 200 205
Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
210 215 220
Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
225 230 235 240
Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
245 250 255
His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
260 265 270

Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
 275 280 285
 Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
 290 295 300
 Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
 305 310 315 320
 Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
 325 330 335
 Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
 340 345 350
 Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
 355 360 365
 Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
 370 375 380
 Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
 385 390 395 400
 Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
 405 410 415
 Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
 420 425 430
 Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
 435 440 445
 Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
 450 455 460
 Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
 465 470 475 480
 Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
 485 490 495
 Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
 500 505 510
 Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
 515 520 525
 Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
 530 535 540
 Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
 545 550 555 560
 Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
 565 570 575
 Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
 580 585 590
 Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 595 600 605

Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 610 615 620
 Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg
 625 630 635 640
 Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met
 645 650 655
 Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly
 660 665 670
 Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
 675 680 685
 Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe
 690 695 700
 Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn
 705 710 715 720
 Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro
 725 730 735
 Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr
 740 745 750
 Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro
 755 760 765
 Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu
 770 775 780
 Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu
 785 790 795 800
 Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
 805 810 815
 Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met
 820 825 830
 Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile
 835 840 845
 Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn
 850 855 860
 Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr
 865 870 875 880
 Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met
 885 890 895
 Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe
 900 905 910
 Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr
 915 920 925
 Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala
 930 935 940

Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val
 945 950 955 960

Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile
 965 970 975

Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His
 980 985 990

Phe Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
 995 1000 1005

Met Ile Leu Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln
 1010 1015 1020

Ser Leu Ile Gln Tyr Asp Ala
 1025 1030

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCAAAACC CCAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG GTAGTTTAGA	60
AATAAAATAT TATTCCTGCA CAAATGGAGA TGGATATTGA TTTGGATGAT ATAGAAAATT	120
TACTTCCTAA TACATTCAAC AAGTATAGCA GCTCTTGTAG TGACAAGAAA GGATGCAAAA	180
CATTGAAATC TGGCTCGAAA TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG	240
AGTTCTACTT CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA	300
AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA AATCAGGTAA	360
TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA TTATGGAGAA AATTACTTAA	420
TACTAAAAGG TAAACAGTTT GGATTATTTT CCTAGCCAAC AATGATGAGT ATATTAAATT	480
CATATGAGAA TGAGTCAAAG GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT	540
AAAACGCAAG AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCTG	600
TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC TTGAGACAAT	660
TGAAAAAGCT GTTTACAACG GAAGGAATCG CAGTTCTGAA AGTTCTGATG TGTATGCCAT	720
TATTTTGTGA ATTAATCTCA AATATCTTAT CTCAATTTAA TGGATAGCTA TAGAAACAAA	780
CCAAATAAAC CATGCAAGTT TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC	840
TGAATTTATA TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC	900
TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT AAAAGAAGCA	960

GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAT TTGTTGATTC TTCTGTAACC 1020
 GGAATTAACA ACAAGAATAT TAGCAACGAA AAAGAAGAAG AGCTATCACA ATCCTGATTC 1080
 TTAAAGATTT CAAAAATTCC AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG 1140
 TTTTTCATTT CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA 1200
 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT TCACATTCAT 1260
 AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA GCAGTCATCC GTTTTAAAAA 1320
 TAGTGCTATG AGGACTAAAT TTTTAGAGTC AAGAAATGGA GCCGAAATCT TAATCAAAAA 1380
 GAATTGCGTC GATATTGCAA AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA 1440
 ATCTTGATTG ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA 1500
 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG CGATCTTCAA 1560
 TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA ATACAAACCT TGGTCAAAAT 1620
 ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA AAAGAAAAAA TAAGGCAATA AATAAAATGA 1680
 GTACAGAAGT GAAGAAATAA AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT 1740
 TTGGGGTTTTT GGGGTTTTTG GG 1762

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro	Gln	Asn	Pro	Lys	Thr	Pro	Lys	Pro	Leu	Lys	Lys	Lys	Lys	Leu	Arg
1				5					10					15	
Phe	Arg	Asn	Lys	Ile	Leu	Phe	Pro	His	Lys	Trp	Arg	Trp	Ile	Leu	Ile
			20					25					30		
Trp	Met	Ile	Lys	Ile	Tyr	Phe	Leu	Ile	His	Ser	Thr	Ser	Ile	Ala	Ala
			35				40					45			
Leu	Val	Val	Thr	Arg	Lys	Asp	Ala	Lys	His	Cys	Asn	Leu	Ala	Arg	Asn
			50			55					60				
Arg	Leu	His	Cys	Leu	Phe	Gln	Ser	Cys	Lys	Asn	Asn	Ser	Ser	Thr	Ser
65				70					75					80	
Arg	Met	Gln	Ile	Phe	Ile	Thr	Ile	Leu	Ser	Cys	Glu	Asn	Phe	Lys	Ala
			85					90						95	
Glu	Ser	Lys	Glu	Lys	Leu	Lys	His	Tyr	Cys	Leu	Asn	Lys	Ile	Arg	Cys
			100					105					110		
Gly	Leu	Phe	Tyr	Phe	Leu	Asp	His	Phe	Leu	Arg	Ser	Ile	Met	Glu	Lys

115					120					125					
Ile	Thr	Tyr	Lys	Val	Asn	Ser	Leu	Asp	Tyr	Phe	Pro	Ser	Gln	Gln	Cys
130					135					140					
Cys	Val	Tyr	Ile	His	Met	Arg	Met	Ser	Gln	Arg	Ile	Ser	Ile	His	Gln
145					150					155					160
Thr	Tyr	Gln	Arg	Gln	Thr	Arg	Tyr	Lys	Thr	Gln	Glu	Lys	Val	Cys	Ser
				165					170					175	
Asn	Ser	Arg	Arg	Thr	Tyr	Cys	Ile	Tyr	Tyr	Ser	Tyr	Gly	Phe	Tyr	Tyr
				180				185					190		
Asn	Cys	Phe	Arg	Tyr	Arg	Arg	Cys	Thr	Pro	Glu	Ser	Cys	Asp	Asn	Cys
		195					200					205			
Lys	Ser	Cys	Leu	Gln	Leu	Lys	Glu	Ser	Gln	Phe	Cys	Lys	Phe	Cys	Val
	210					215					220				
Cys	His	Tyr	Phe	Val	Asn	Ser	Gln	Ile	Ser	Tyr	Leu	Asn	Leu	Met	Asp
225					230					235					240
Ser	Tyr	Arg	Asn	Lys	Pro	Asn	Lys	Pro	Cys	Lys	Phe	Asn	Gly	Ile	Tyr
				245					250					255	
Val	Lys	Ser	Phe	Gly	Thr	Asn	Ala	His	Cys	Ile	Tyr	Ile	Gly	Phe	Leu
			260					265					270		
Lys	His	Arg	Tyr	Thr	Glu	Cys	Phe	Arg	Asp	Cys	Phe	Ser	Leu	Gln	Gln
		275					280					285			
Ile	Thr	Cys	Phe	Asp	Tyr	Ser	Cys	Ser	Ser	Leu	Ile	Ser	Leu	Lys	Glu
	290					295					300				
Ala	Gly	Glu	Met	Lys	Arg	Arg	Leu	Lys	Lys	Glu	Ile	Ser	Lys	Phe	Val
305					310					315					320
Asp	Ser	Ser	Val	Thr	Gly	Ile	Asn	Asn	Lys	Asn	Ile	Ser	Asn	Glu	Lys
				325					330					335	
Glu	Glu	Glu	Leu	Ser	Gln	Ser	Cys	Phe	Leu	Lys	Ile	Ser	Lys	Ile	Pro
			340					345					350		
Gly	Lys	Arg	Asp	Thr	Phe	Ile	Lys	Ile	His	Ile	Leu	Phe	Phe	Ile	Ser
		355					360					365			
Gln	Leu	Leu	Phe	Ser	Phe	Ile	Leu	Thr	Ile	Phe	Phe	Asp	Leu	Glu	Val
	370					375					380				
Lys	Ser	Ile	Lys	Glu	Lys	Arg	Thr	Glu	Val	Thr	Leu	Ile	His	Ile	His
385					390					395					400
Arg	Ser	Thr	Phe	Ile	Tyr	Pro	Ile	Arg	Cys	Gly	Asn	Ser	Ser	His	Pro
				405					410					415	
Phe	Lys	Cys	Tyr	Glu	Asp	Ile	Phe	Arg	Val	Lys	Lys	Trp	Ser	Arg	Asn
			420					425					430		
Leu	Asn	Gln	Lys	Glu	Leu	Arg	Arg	Tyr	Cys	Lys	Arg	Ile	Glu	Leu	Ile
		435					440					445			

Phe Arg Val Leu Pro Ile Leu Ile Asp Cys Arg Asp Arg Gly Asn Cys
 450 455 460
 Thr Glu Asp His Arg Asn Lys Val Thr Phe Ile Asn Arg Ile Asn Ile
 465 470 475 480
 Thr Asn Ile Glu Ile Ser Asp Leu Gln Leu Thr Lys Lys Leu Asn Ser
 485 490 495
 Thr Ile Lys Asn Thr Asn Leu Gly Gln Asn Ile Glu Glu Gly Lys Glu
 500 505 510
 Asp Gln Leu Ala Lys Glu Lys Ile Arg Gln Ile Lys Cys Val Gln Lys
 515 520 525
 Cys Arg Asn Lys Arg Phe Ile Phe Phe Asn Asn Leu Leu Lys Arg Gly
 530 535 540
 Val Leu Gly Phe Trp Gly Phe Gly
 545 550

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 562 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Pro Lys Thr Pro Lys Pro Gln Asn Pro Tyr Lys Lys Arg Lys Asn Cys
 1 5 10 15
 Gly Ser Leu Glu Ile Lys Tyr Tyr Ser Arg Thr Asn Gly Asp Gly Tyr
 20 25 30
 Cys Phe Gly Cys Tyr Arg Lys Phe Thr Ser Tyr Ile Gln Gln Val Gln
 35 40 45
 Leu Leu Gln Glu Arg Met Gln Asn Ile Glu Ile Trp Leu Glu Ile Ala
 50 55 60
 Phe Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg Val Leu Leu Leu
 65 70 75 80
 Gly Cys Lys Ser Leu Arg Phe Phe Leu Glu Lys Ile Ser Phe Lys Lys
 85 90 95
 Arg Arg Ala Lys Ser Arg Asn Cys Asn Ile Thr Asn Val Ile Lys Ser
 100 105 110
 Gly Asn Glu Asp Tyr Ser Ile Phe Ile Thr Ser Gly Ala Leu Trp Arg
 115 120 125
 Lys Leu Leu Asn Thr Lys Arg Thr Val Trp Ile Ile Ser Leu Ala Asn
 130 135 140
 Asn Asp Glu Tyr Ile Lys Phe Ile Cys Glu Cys Val Lys Gly Ser Arg
 145 150 155 160

Tyr Ile Arg Leu Thr Lys Asp Lys Leu Ala Ile Lys Arg Lys Lys Lys
165 170 175
Phe Asp Asn Arg Thr Ala Glu Glu Leu Ile Ala Phe Thr Ile Arg Met
180 185 190
Gly Phe Ile Thr Ile Val Leu Gly Ile Asp Gly Glu Leu Pro Ser Leu
195 200 205
Glu Thr Ile Glu Lys Ala Val Tyr Asn Cys Arg Asn Arg Ser Ser Glu
210 215 220
Ser Ser Asp Val Tyr Ala Ile Ile Leu Cys Ile Asn Leu Lys Tyr Leu
225 230 235 240
Ile Ser Ile Trp Ile Ala Ile Glu Thr Asn Gln Ile Asn His Ala Ser
245 250 255
Leu Met Glu Tyr Thr Leu Asn Pro Leu Gly Gln Met His Thr Glu Phe
260 265 270
Ile Leu Asp Ser Ser Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu
275 280 285
Ala Tyr Asn Arg Leu Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr
290 295 300
Leu Lys Lys Gln Ala Lys Cys Lys Glu Asp Arg Lys Arg Phe Gln Asn
305 310 315 320
Leu Leu Ile Leu Leu Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys
325 330 335
Lys Lys Lys Ser Tyr His Asn Pro Asp Ser Arg Phe Gln Lys Phe Gln
340 345 350
Val Arg Glu Ile His Ser Leu Lys Phe Ile Tyr Tyr Ser Phe Ser Phe
355 360 365
His Ser Cys Tyr Phe Leu Leu Ser Gln Tyr Phe Leu Ile Ser Trp Lys
370 375 380
Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg Leu Ser Leu Phe Thr
385 390 395 400
Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp Asp Lys Glu Thr Ala
405 410 415
Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr Lys Phe Leu Glu Ser
420 425 430
Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn Cys Val Asp Ile Ala
435 440 445
Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys Tyr Tyr Gln Ser Cys
450 455 460
Leu Ile Glu Glu Ile Asp Glu Ala Thr Ala Gln Lys Ile Ile Lys Glu
465 470 475 480
Ile Lys Leu Leu Leu Ile Arg Glu Thr Lys Leu Leu Ile Arg Ser Ala
485 490 495

Ile Phe Asn Cys Arg Asn Lys Ser Cys Thr Lys Val Arg Gln Lys Ile
500 505 510

Gln Thr Leu Val Lys Ile Leu Arg Lys Glu Lys Lys Thr Ser Gln Lys
515 520 525

Lys Lys Gly Asn Lys Asn Glu Tyr Arg Ser Glu Glu Ile Lys Asp Leu
530 535 540

Phe Phe Ser Ile Ile Tyr Cys Lys Glu Gly Phe Trp Gly Phe Gly Val
545 550 555 560

Leu Gly

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Lys Pro Gln Asn Pro Lys Thr Pro Ile Lys Lys Glu Lys Ile Glu
1 5 10 15

Val Val Lys Asn Ile Ile Pro Ala Gln Met Glu Met Asp Ile Asp Leu
20 25 30

Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn Lys Tyr Ser Ser
35 40 45

Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys Ser Gly Ser Lys
50 55 60

Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln Leu Glu Phe Tyr
65 70 75 80

Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu Arg Lys Leu Val
85 90 95

Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr Leu Leu Met Phe
100 105 110

Lys Asn Gln Val Met Arg Ile Ile Leu Phe Phe Arg Ser Leu Leu Lys
115 120 125

Glu His Tyr Gly Glu Asn Tyr Leu Ile Leu Lys Gly Lys Gln Phe Gly
130 135 140

Leu Phe Pro Pro Thr Met Met Ser Ile Leu Asn Ser Tyr Glu Asn Glu
145 150 155 160

Ser Lys Asp Leu Asp Thr Ser Asp Leu Pro Lys Thr Asn Ser Leu Asn
165 170 175

Ala Arg Lys Ser Leu Ile Ile Glu Gln Lys Asn Leu Leu His Leu
180 185 190

Leu Phe Val Trp Val Leu Leu Gln Leu Phe Val Ser Thr Val Asn Ser
 195 200 205
 Arg Val Leu Arg Gln Leu Lys Lys Leu Phe Thr Thr Glu Gly Ile Ala
 210 215 220
 Val Leu Lys Val Leu Met Cys Met Pro Leu Phe Cys Glu Leu Ile Ser
 225 230 235 240
 Asn Ile Leu Ser Gln Phe Asn Gly Leu Lys Gln Thr Lys Thr Met Gln
 245 250 255
 Val Trp Asn Ile Arg Ile Leu Trp Asp Lys Cys Thr Leu Asn Leu Tyr
 260 265 270
 Trp Ile Leu Lys Ala Ile His Arg Met Leu Arg Leu Ile Leu Thr Thr
 275 280 285
 Asp Tyr Leu Phe Cys Leu Leu Leu Leu Ile Ser Tyr Ile Phe Lys Arg
 290 295 300
 Ser Arg Arg Asn Glu Lys Lys Thr Lys Glu Arg Asp Phe Lys Ile Cys
 305 310 315 320
 Cys Phe Phe Cys Asn Arg Asn Gln Gln Glu Tyr Gln Arg Lys Arg Arg
 325 330 335
 Arg Ala Ile Thr Ile Leu Ile Leu Lys Asp Phe Lys Asn Ser Arg Glu
 340 345 350
 Arg Tyr Ile His Asn Ser Tyr Ile Ile Val Phe His Phe Thr Ala Val
 355 360 365
 Ile Phe Phe Tyr Leu Asn Asn Ile Phe Cys Leu Ala Gly Ser Lys Lys
 370 375 380
 Tyr Gln Ile Arg Glu Ala Leu Asp Cys Gly Asn Leu Ala Tyr Ser His
 385 390 395 400
 Ser Ile Asp Leu His Ile Ser Asn Thr Met Ile Arg Lys Gln Gln Ser
 405 410 415
 Ser Val Leu Lys Ile Val Leu Cys Gly Leu Asn Phe Ser Gln Glu Met
 420 425 430
 Glu Pro Lys Ser Ser Lys Arg Ile Ala Ser Ile Leu Gln Lys Asn Arg
 435 440 445
 Thr Leu Asn Leu Ser Leu Ile Ser Ile Thr Asn Leu Asp Cys Leu Lys
 450 455 460
 Arg Leu Thr Arg Gln Leu His Arg Arg Ser Leu Lys Lys Ser Asn Phe
 465 470 475 480
 Tyr Leu Glu Asn Lys Leu Asn Tyr Tyr Arg Asp Gln Arg Ser Ser Ile
 485 490 495
 Asp Glu Ile Lys Ala Glu Leu Lys Leu Asp Asn Lys Lys Tyr Lys Pro
 500 505 510
 Trp Ser Lys Tyr Cys Gly Arg Lys Arg Arg Pro Val Ser Lys Arg Lys
 515 520 525

Asn Lys Ala Ile Asn Lys Met Ser Thr Glu Val Lys Lys Lys Ile Tyr
530 535 540

Phe Phe Gln Phe Ile Glu Lys Arg Gly Phe Gly Val Leu Gly Phe Trp
545 550 555 560

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Glu	Ile	Glu	Asn	Asn	Gln	Ala	Gln	Gln	Pro	Lys	Ala	Glu	Lys	Leu	1	5	10	15
Trp	Trp	Glu	Leu	Glu	Leu	Glu	Met	Gln	Glu	Asn	Gln	Asn	Asp	Ile	Gln	20	25	30	
Val	Arg	Val	Lys	Ile	Asp	Asp	Pro	Lys	Gln	Tyr	Leu	Val	Asn	Val	Thr	35	40	45	
Ala	Ala	Cys	Leu	Leu	Gln	Glu	Gly	Ser	Tyr	Tyr	Gln	Asp	Lys	Asp	Glu	50	55	60	
Arg	Arg	Tyr	Ile	Ile	Thr	Lys	Ala	Leu	Leu	Glu	Val	Ala	Glu	Ser	Asp	65	70	75	80
Pro	Glu	Phe	Ile	Cys	Gln	Leu	Ala	Val	Tyr	Ile	Arg	Asn	Glu	Leu	Tyr	85	90	95	
Ile	Arg	Thr	Thr	Thr	Asn	Tyr	Ile	Val	Ala	Phe	Cys	Val	Val	His	Lys	100	105	110	
Asn	Thr	Gln	Pro	Phe	Ile	Glu	Lys	Tyr	Phe	Asn	Lys	Ala	Val	Leu	Leu	115	120	125	
Pro	Asn	Asp	Leu	Leu	Glu	Val	Cys	Glu	Phe	Ala	Gln	Val	Leu	Tyr	Ile	130	135	140	
Phe	Asp	Ala	Thr	Glu	Phe	Lys	Asn	Leu	Tyr	Leu	Asp	Arg	Ile	Leu	Ser	145	150	155	160
Gln	Asp	Ile	Arg	Lys	Glu	Leu	Thr	Phe	Arg	Lys	Cys	Leu	Gln	Arg	Cys	165	170	175	
Val	Arg	Ser	Lys	Phe	Ser	Glu	Phe	Asn	Glu	Tyr	Gln	Leu	Gly	Lys	Tyr	180	185	190	
Cys	Thr	Glu	Ser	Gln	Arg	Lys	Lys	Thr	Met	Phe	Arg	Tyr	Leu	Ser	Val	195	200	205	
Thr	Asn	Lys	Gln	Lys	Trp	Asp	Gln	Thr	Lys	Lys	Lys	Arg	Lys	Glu	Asn	210	215	220	
Leu	Leu	Thr	Lys	Leu	Gln	Ala	Ile	Lys	Glu	Ser	Glu	Asp	Lys	Ser	Lys	225	230	235	240

Arg Glu Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu
 245 250 255
 Lys Pro Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys
 260 265 270
 Lys His Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys
 275 280 285
 Tyr Leu Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro
 290 295 300
 Lys Glu Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu
 305 310 315 320
 Glu Glu Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn
 325 330 335
 Pro Glu Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp
 340 345 350
 Glu Asn Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn
 355 360 365
 Leu Ile Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu
 370 375 380
 Ser Asn Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val
 385 390 395 400
 Ile Asn Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe
 405 410 415
 Pro Leu Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr
 420 425 430
 Lys Gly Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln
 435 440 445
 Ile Glu Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys
 450 455 460
 Asp Met Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn
 465 470 475 480
 Glu Gly Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys
 485 490 495
 Ile Ala Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile
 500 505 510
 Phe Ser Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala
 515 520 525
 Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu
 530 535 540
 Gly Leu Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe
 545 550 555 560
 Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu
 565 570 575

Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys
 580 585 590
 Gly Lys Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu
 595 600 605
 Trp Thr Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp
 610 615 620
 Met Met Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser
 625 630 635 640
 Ile Val Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile
 645 650 655
 Lys Ile Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu
 660 665 670
 Gly Asp Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser
 675 680 685
 Asp Ser Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met
 690 695 700
 Val Glu Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly Gln Lys
 705 710 715

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu
 1 5 10 15
 Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln
 20 25 30
 Ile Glu His Tyr Lys Thr Gln Gln Gln Ile Lys Glu Glu Asp Leu
 35 40 45
 Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80
 Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
 85 90 95
 Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
 100 105 110
 Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
 115 120 125

Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp
 130 135 140
 Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg
 145 150 155 160
 Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln
 165 170 175
 Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp
 180 185 190
 Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val
 195 200 205
 Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
 210 215 220
 Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
 225 230 235 240
 Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
 245 250 255
 Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
 260 265 270
 Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
 275 280 285
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
 290 295 300
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
 305 310 315 320
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
 325 330 335
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
 340 345 350
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
 355 360 365
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
 370 375 380
 Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn
 385 390 395 400
 Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
 405 410 415
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
 420 425 430
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
 435 440 445
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
 450 455 460

Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
 465 470 475 480
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
 485 490 495
 Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
 500 505 510
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
 515 520 525
 Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met
 530 535 540
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu
 545 550 555 560
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His
 565 570 575
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys
 580 585 590
 Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe
 595 600 605
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu
 610 615 620
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser
 625 630 635 640
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu
 645 650 655
 Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu
 660 665 670
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser
 675 680 685
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe
 690 695 700
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr
 705 710 715 720
 Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800

Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
805 810 815

Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
820 825 830

Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu
835 840 845

Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr
850 855 860

Tyr Asp Tyr Asn Ser Asp Arg Trp
865 870

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn
1 5 10 15

Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys
20 25 30

Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln
35 40 45

Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu
50 55 60

Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr
65 70 75 80

Leu Leu Met

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser Leu Glu Ser Leu Glu
1 5 10 15

Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser Cys Lys Asn Leu Gln
20 25 30

Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro Asn Asn Ile Gln Lys
35 40 45

Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe Lys Gln Phe Glu Gln
50 55 60

Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys Ile Leu Asp Gln His
65 70 75 80

Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys Asn Lys Lys Ile Lys
85 90 95

Ala Phe Ile Leu
100

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Met Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn
1 5 10 15

Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys
20 25 30

Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu
35 40 45

Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp
50 55 60

Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu
65 70 75 80

Ile Glu Thr Leu Leu
85

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu Asp Glu Ile
1 5 10 15

Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser Met Ser Thr
20 25 30

Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu
35 40 45

Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg Cys Glu Lys
50 55 60

Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys Lys Cys Tyr
65 70 75 80

Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys
85 90 95

Leu Leu

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
1 5 10 15

Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
20 25 30

Leu Leu Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys
35 40 45

Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser
50 55 60

Ser Leu Gly Phe Leu
65

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Asn Arg Asn Leu His Cys Thr Tyr Ile Asp Tyr Lys Lys Ala Phe
1 5 10 15

Asp Ser Ile Pro His Ser Trp Leu Ile Gln Val Leu Glu Ile Tyr Lys
20 25 30

Ile Asn Arg Gln Ile Ala Ile Lys Lys Gly Ile Tyr Gln Gly Asp Ser
35 40 45

Leu Ser Pro Leu Trp Phe Cys Leu Ala Leu Asn Pro Leu Ser His Gln
 50 55 60

Leu His Asn Asp Arg
 65

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Gly Gly Ser Asn Trp Phe Arg Glu Val Asp Leu Lys Lys Cys Phe
 1 5 10 15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
 20 25 30

Ser Asp His Val Pro Val Gly Pro Arg Val Cys Val Gln Gly Ala Pro
 35 40 45

Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu Asp Arg Arg
 50 55 60

Leu Ala Gly Leu Ala
 65

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr
 1 5 10 15

Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr
 20 25 30

Ile Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys
 35 40 45

Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro
 50 55 60

Phe Arg Lys Gln Asn
 65

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
1 5 10 15
Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu
 20 25 30
Lys Asn Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser
 35 40 45
Leu Ser Ala Pro Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe
50 55 60
Tyr Ser Glu Phe Lys
65

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn
1 5 10 15
Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu Asn
 20 25 30
Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Gln Asp Tyr Cys Asp
35 40 45
Trp Ile Gly Ile Ser Ile
50

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Leu Ile Tyr Met Asp Asp Ile Lys Leu Tyr Ala Lys Asn Asp Lys
1 5 10 15
Glu Met Lys Lys Leu Ile Asp Thr Thr Thr Ile Phe Ser Asn Asp Ile
20 25 30
Ser Met Gln Phe Gly Leu Asp Lys Cys Lys Thr Lys Cys Leu Tyr Lys
35 40 45
Tyr Leu Gly Phe Gln Gln
50

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Val Arg Tyr Ala Asp Asp Ile Leu Ile Gly Val Leu Gly Ser Lys
1 5 10 15
Asn Lys Ile Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly
20 25 30
Leu Thr Ile Asn Glu Glu Lys Thr Leu Ile Glu Thr Pro Ala Arg Phe
35 40 45
Leu Gly Tyr Asn Ile
50

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser His Leu Glu Ile
1 5 10 15
Gly His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp
20 25 30
Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu
35 40 45
Trp Met Gly Tyr Glu Leu
50

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
1 5 10 15
Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr
20 25 30
Asn Ala Lys Ala Asn Arg Ile Arg Ser Lys Ser Ser Lys Gly Ile Phe
35 40 45
Arg

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn
1 5 10 15
Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val
20 25 30
Glu Ile Glu Thr Leu Leu Met
35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile Cys His Gln Glu Tyr Tyr Phe Gly Asp Phe Asn Leu Pro Arg Asp
1 5 10 15
Lys Phe Leu Lys Glu Gln Ile Lys Leu Asp Glu Gly Trp Val Pro Leu
20 25 30
Glu Ile Met Ile Lys
35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile Cys Glu Gln Ile Glu Tyr Tyr Phe Gly Asp His Asn Leu Pro Arg
1 5 10 15
Asp Lys Phe Leu Lys Gln Gln Ile Leu Leu Asp Asp Gly Trp Val Pro
20 25 30
Leu Glu Thr Met Ile Lys
35

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile Leu Arg Gln Val Glu Tyr Tyr Phe Gly Asp Ala Asn Leu Asn Arg
1 5 10 15
Asp Lys Phe Leu Arg Glu Gln Ile Gly Lys Asn Glu Asp Gly Trp Val
20 25 30
Pro Leu Ser Val Leu Val Thr
35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Leu Lys Gln Val Glu Phe Tyr Phe Ser Glu Phe Asn Phe Pro Tyr
1 5 10 15
Asp Arg Phe Leu Arg Thr Thr Ala Glu Lys Asn Asp Gly Trp Val Pro
20 25 30
Ile Ser Thr Ile Ala Thr
35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TAGACCTGTT AGTGACATT TGAATTGAAG C

31

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAAAACCCCA AAACCTAACA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCGGGAATTC TAATACGACT CACTATAGGG AAGAACTCT GATGAGGCCG AAAGGCCGAA 60

ACTCCACGAA AGTGGAGTAA GTTCTCGAT AATTGATCTG TAG 103

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGATCCT CTTCAAAAAGA TGAGAGGACA GCAAAC 36

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCAAAACC CAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTTGG GGTTTTGGGG 60

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAAAACCCC AAAACCCCCA AACCCCCACA GGGGTTTTGG GGTTTTGGGG TTTTGGGG 58

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAAACCCCAA AACCCCAAAA CCCCACAGG GGTTTTGGGG TTTGGGGTT TTGGGG

56

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTGGGGTT TTGGGGTTTT GGGG

54

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCCCAAAACC CAAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAAACCCCAA AACCCCAAAA CCCCACAGG GGTTTTGGGG TTTGGGGTT TT

52

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT

50

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCCAAACC CCAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAAACCCC AAAACCCCA CAGGGGTTTT GGGGTTTTGG GGTITT

46

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAACCCCAA AACCCCA CAGGGGTTTTGG GGTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "RNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTTGGGG

8

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "RNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGGGTTTT

8

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCTRAARTAR TGDGTNADRT TRTTCAT

27

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCGGATCCAT GAAYCCWGAR AAYCCWAAYG T

31

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

NNNGTNACHG GHATHAAYAA

20

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

DGCDGTYTCY TGRTCTTTRT A

21

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AACTCATTTA ATTACTAATT TAATCAACAA GATTGATAAA AAGCAGTAAA TAAAACCCAA 60
TAGATTTAAT TTAGAAAGTA TCAATTGAAA AATGGAAATT GAAAACAACT AAGCACAATA 120
GCCAAAAGCC GAAAAATTGT GGTGGGAACT TGAATTAGAG ATGCAAGAAA ACCAAAATGA 180
TATATAAGTT AGGGTTAAGA TTGACGATCC TAAGCAATAT CTCGTGAACG TCACTGCAGC 240
ATGTTTGTTG TAGGAAGGTA GTTACTACTA AGATAAAGAT GAAAGAAGAT ATATCATCAC 300
TAAAGCACTT CTTGAGGTGG CTGAGTCTGA TCCTGAGTTC ATCTGCTAGT TGGCAGTCTA 360
CATCCGTAAT GAACTTTACA TCAGAACTAC CACTAACTAC ATTGTAGCAT TTTGTGTTGT 420
CCACAAGAAT ACTCAACCAT TCATCGAAAA GTACTTCAAC AAAGCAGTAC TTTTGCCTAA 480
TGACTTACTG GAAGTCTGTG AATTTGCATA GGTCTCTAT ATTTTGTATG CAACTGAATT 540
CAAAAATTTG TATCTTGATA GGATACTTTC ATAAGATATT CGTAAGGAAC TCACTTTCCG 600
TAAGTGTTTA CAAAGATGCG TCAGAAGCAA GTTTTCTGAA TTCAACGAAT ACTAAGTTGG 660
TAAGTATTGC ACTGAATCCT AACGTAAGAA AACAATGTTC CGTTACCTCT CAGTTACCAA 720
CAAGTAAAAG TGGGATTAAA CTAAGAAGAA GAGAAAAGAG AATCTCTTAA CCAAACTTTA 780
GGCAATAAAG GAATCTGAAG ATAAGTCCAA GAGAGAAACT GGAGACATAA TGAACGTTGA 840
AGATGCAATC AAGGCTTTAA AACCAGCAGT TATGAAGAAA ATAGCCAAGA GATAGAATGC 900
CATGAAGAAA CACATGAAGG CACCTAAAAT TCCTAACTCT ACCTTGGAAT CAAAGTACTT 960
GACCTTCAAG GATCTCATT AGTTCTGCCA TATTTCTGAG CCTAAAGAAA GAGTCTATAA 1020
GATCCTTGGT AAAAAATACC CTAAGACCGA AGAGGAATAC AAAGCAGCCT TTGGTGATTCT 1080
TGCATCTGCA CCCTTCAATC CTGAATTGGC TGGAAAGCGT ATGAAGATTG AAATCTCTAA 1140
AACATGGGAA AATGAACTCA GTGCAAAGG CAACACTGCT GAGGTTTGGG ATAATTTAAT 1200
TTCAAGCAAT TAACTCCCAT ATATGGCCAT GTTACGTAAC TTGTCTAACA TCTTAAAAGC 1260
CGGTGTTTCA GATACTACAC ACTCTATTGT GATCAACAAG ATTTGTGAGC CCAAGGCCGT 1320
TGAGAACTCC AAGATGTTCC CTCTTCAATT CTTTAGTGCC ATTGAAGCTG TTAATGAAGC 1380
AGTTACTAAG GGATTCAAGG CCAAGAAGAG AGAAAATATG AATCTTAAAG GTCAAATCGA 1440
AGCAGTAAAG GAAGTTGTTG AAAAAACCGA TGAAGAGAAG AAAGATATGG AGTTGGAGTA 1500

AACCGAAGAA GGAGAATTTG TTAAAGTCAA CGAAGGAATT GGCAAGCAAT ACATTAACTC	1560
CATTGAACTT GCAATCAAGA TAGCAGTTAA CAAGAATTTA GATGAAATCA AAGGACACAC	1620
TGCAATCTTC TCTGATGTTT CTGGTTCTAT GAGTACCTCA ATGTCAGGTG GAGCCAAGAA	1680
GTATGGTTCC GTTCGTACTT GTCTCGAGTG TGCATTAGTC CTTGGTTTGA TGGTAAAATA	1740
ACGTTGTGAA AAGTCCTCAT TCTACATCTT CAGTTCACCT AGTTCTCAAT GCAATAAGTG	1800
TTACTTAGAA GTTGATCTCC CTGGAGACGA ACTCCGTCCT TCTATGTAAA AACTTTTGCA	1860
AGAGAAAGGA AACTTGGTG GTGGTACTGA TTTCCCTAT GAGTGCATTG ATGAATGGAC	1920
AAAGAATAAA ACTCACGTAG ACAATATCGT TATTTTGTCT GATATGATGA TTGCAGAAGG	1980
ATATTCAGAT ATCAATGTTA GAGGCAGTTC CATTGTTAAC AGCATCAAAA AGTACAAGGA	2040
TGAAGTAAAT CCTAACATTA AAATCTTTGC AGTTGACTTA GAAGGTTACG GAAAGTGCCT	2100
TAATCTAGGT GATGAGTTCA ATGAAAACAA CTACATCAAG ATATTCGGTA TGAGCGATTG	2160
AATCTTAAAG TTCATTTTCA CCAAGCAAGG AGGAGCAAAT ATGGTCGAAG TTATCAAAAA	2220
CTTTGCCCTT CAAAAATAG GACAAAAGTG AGTTTCTTGA GATTCTTCTA TAACAAAAAT	2280
CTCACCCAC TTTTTGTTT TATTGCATAG CCATTATGAA ATTTAAATTA TTATCTATTT	2340
ATTTAAGTTA CTTACATAGT TTATGTATCG CAGTCTATTA GCCTATTCAA ATGATTCTGC	2400
AAAGAACAAA AAAGATTAAA A	2421

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Glu	Leu	Glu	Leu	Glu	Met	Gln	Glu	Asn	Gln	Asn	Asp	Ile	Gln	Val	Arg
1				5					10					15	
Val	Lys	Ile	Asp	Asp	Pro	Lys	Gln	Tyr	Leu	Val	Asn	Val	Thr	Ala	Ala
			20					25					30		
Cys	Leu	Leu	Gln	Glu	Gly	Ser	Tyr	Tyr	Gln	Asp	Lys	Asp	Glu	Arg	Arg
			35				40					45			
Tyr	Ile	Ile	Thr	Lys	Ala	Leu	Glu	Val	Ala	Glu	Ser	Asp	Pro	Glu	
			50			55				60					
Phe	Ile	Cys	Gln	Leu	Ala	Val	Tyr	Ile	Arg	Asn	Glu	Leu	Tyr	Ile	Arg
65				70					75					80	
Thr	Thr	Thr	Asn	Tyr	Ile	Val	Ala	Phe	Cys	Val	Val	His	Lys	Asn	Thr
			85						90					95	

Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu Pro Asn
 100 105 110
 Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp
 115 120 125
 Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp
 130 135 140
 Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys Val Arg
 145 150 155 160
 Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr Cys Thr
 165 170 175
 Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val Thr Asn
 180 185 190
 Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn Leu Leu
 195 200 205
 Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys Arg Glu
 210 215 220
 Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro
 225 230 235 240
 Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His
 245 250 255
 Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu
 260 265 270
 Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu
 275 280 285
 Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu Glu Glu
 290 295 300
 Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu
 305 310 315 320
 Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn
 325 330 335
 Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile
 340 345 350
 Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn
 355 360 365
 Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val Ile Asn
 370 375 380
 Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu
 385 390 395 400

Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly
 405 410 415
 Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu
 420 425 430
 Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met
 435 440 445
 Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly
 450 455 460
 Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala
 465 470 475 480
 Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser
 485 490 495
 Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys
 500 505 510
 Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu
 515 520 525
 Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser
 530 535 540
 Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly
 545 550 555 560
 Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys
 565 570 575
 Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr
 580 585 590
 Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp Met Met
 595 600 605
 Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val
 610 615 620
 Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile
 625 630 635 640
 Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp
 645 650 655
 Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser
 660 665 670
 Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu
 675 680 685
 Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly
 690 695

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2829 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCAATACTAT TAATTAATAA ATAAAAA GCAAACTACA AAGAAAATGT CAAGGCGTAA	60
CTAAAAAAG CCATAGGCTC CTATAGGCAA TGAAACAAAT CTTGATTTTG TATTACAAAA	120
TCTAGAAGTT TACAAAAGCC AGATTGAGCA TTATAAGACC TAGTAGTAAT AGATCAAAGA	180
GGAGGATCTC AAGCTTTTAA AGTTCAAAAA TTAAGATTAG GATGGAAACT CTGGCAACGA	240
TGATGATGAT GAAGAAAACA ACTCAAATAA ATAATAAGAA TTATTAAGGA GAGTCAATTA	300
GATTAAGTAG CAAGTTTAAT TGATAAAAA AGTTGGTTCT AAGGTAGAGA AAGATTGAA	360
TTTGAACGAA GATGAAAACA AAAAGAATGG ACTTTCTGAA TAGCAAGTGA AAGAAGAGTA	420
ATTAAGAACG ATTACTGAAG AATAGGTTAA GTATTAAAAT TTAGTATTTA ACATGGACTA	480
CCAGTTAGAT TTAAATGAGA GTGGTGGCCA TAGAAGACAC AGAAGAGAAA CAGATTATGA	540
TACTGAAAAA TGGTTTGAAA TATCTCATGA CCAAAAAAAT TATGTATCAA TTTACGCCAA	600
CTAAAAGACA TCATATTGTT GGTGGCTTAA AGATTATTTT AATAAAAACA ATTATGATCA	660
TCTTAATGTA AGCATTAAAC GACTAGAAAC TGAAGCCGAA TTCTATGCCT TTGATGATTT	720
TTCACAAACA ATCAAACTTA CTAATAATTC TTACTAGACT GTTAACATAG ACGTTAATTT	780
TGATAATAAT CTCTGTATAC TCGCATTGCT TAGATTTTTA TTATCACTAG AAAGATTCAA	840
TATTTTGAAT ATAAGATCTT CTTATACAAG AAATTAATAT AATTTTGAGA AAATTGGTGA	900
GCTACTTGAA ACTATCTTCG CAGTTGTCTT TTCTCATCGC CACTTACAAG GCATTCATTT	960
ACAAGTTCCT TGCGAAGCGT TCTAATATTT AGTTAACTCC TCATCATAAA TTAGCGTTAA	1020
AGATAGCTAA TTATAGGTAT ACTCTTTCTC TACAGACTTA AAATTAGTTG AACTAACAA	1080
AGTCCAAGAT TATTTTAAGT TCTTATAAGA ATTCCTCGT TTGACTCATG TAAGCTAGTA	1140
GGCTATCCCA GTTAGTGCTA CTAACGCTGT AGAGAACCTC AATGTTTTAC TAAAAAGGT	1200
CAAGCATGCT AATCTTAATT TAGTTTCTAT CCCTACCTAA TTCAATTTTG ATTTCTACTT	1260
TGTTAATTTA TAACATTGTA AATTAGAGTT TGGATTAGAA CCAAATATTT TGACAAAACA	1320
AAAGCTTGAA AATCTACTTT TGAGTATAAA ATAATCAAAA AATCTTAAAT TTTTAAGATT	1380
AACTTTTAC ACCTACGTTG CTTAAGAAAC CTCCAGAAAA CAGATATTAA AACAAGCTAC	1440
AACAATCAAA AATCTCAAAA ACAATAAAAA TCAAGAAGAA ACTCCTGAAA CTAAAGATGA	1500
AACTCCAAGC GAAAGCACAA GTGGTATGAA ATTTTTTGAT CATCTTTCTG AATTAACCGA	1560
GCTTGAAGAT TTCAGCGTTA ACTTGTAAGC TACCCAAGAA ATTTATGATA GCTTGCACAA	1620

ACTTTTGATT AGATCAACAA ATTTAAAGAA GTTCAAATTA AGTTACAAAT ATGAAATGGA 1680
 AAAGAGTAAA ATGGATACAT TCATAGATCT TAAGAATATT TATGAAACCT TAAACAATCT 1740
 TAAAAGATGC TCTGTTAATA TATCAAATCC TCATGGAAAC ATTTCTTATG AACTGACAAA 1800
 TAAAGATTCT ACTTTTTATA AATTTAAGCT GACCTTAAAC TAAGAATTAT AACACGCTAA 1860
 GTATACTTTT AAGTAGAACG AATTTTAATT TAATAACGTT AAAAGTGCAA AAATTGAATC 1920
 TTCCTCATTG GAAAGCTTAG AAGATATTGA TAGTCTTTGC AAATCTATTG CTTCTTGTA 1980
 AAATTTACAA AATGTTAATA TTATCGCCAG TTTGCTCTAT CCCAACAATA TTTAGAAAAA 2040
 TCCTTTCAAT AAGCCCAATC TTCTATTTTT CAAGCAATTT GAATAATTGA AAAATTTGGA 2100
 AAATGTATCT ATCAACTGTA TTCTTGATCA GCATATACTT AATTCTATTT CAGAATTCTT 2160
 AGAAAAGAAT AAAAAAATAA AAGCATTCTT TTTGAAAAGA TATTATTTAT TACAATATTA 2220
 TCTTGATTAT ACTAAATTAT TTAAACACT TCAATAGTTA CCTGAATTAA ATTAAGTTTA 2280
 CATTAATTAG CAATTAGAAG AATTGACTGT GAGTGAAGTA CATAAGTAAG TATGGGAAAA 2340
 CCACAAGCAA AAAGCTTTCT ATGAACCATT ATGTGAGTTT ATCAAAGAAT CATCCTAAAC 2400
 CCTTTAGCTA ATAGATTTTG ACCAAAACAC TGTAAGTGAT GACTCTATTA AAAAGATTTT 2460
 AGAATCTATA TCTGAGTCTA AGTATCATCA TTATTTGAGA TTGAACCCTA GTTAATCTAG 2520
 CAGTTTAATT AAATCTGAAA ACGAAGAAAT TTAAGAACTT CTCAAAGCTT GCGACGAAAA 2580
 AGGTGTTTTA GTAAAAGCAT ACTATAAATT CCCTCTATGT TTACCAACTG GTACTTATTA 2640
 CGATTACAAT TCAGATAGAT GGTGATTAAT TAAATATTAG TTTAAATAAA TATTAAATAT 2700
 TGAATATTTT TTTGCTTATT ATTTGAATAA TACATACAAT AGTCATTTTT AGTGTTTTGA 2760
 ATATATTTTA GTTATTTAAT TCATTATTTT AAGTAAATAA TTATTTTCA ATCATTTTTT 2820
 AAAAAATCG 2829

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ser	Arg	Arg	Asn	Gln	Lys	Lys	Pro	Gln	Ala	Pro	Ile	Gly	Asn	Glu
1				5				10					15		
Thr	Asn	Leu	Asp	Phe	Val	Leu	Gln	Asn	Leu	Glu	Val	Tyr	Lys	Ser	Gln
			20					25					30		
Ile	Glu	His	Tyr	Lys	Thr	Gln	Gln	Gln	Gln	Ile	Lys	Glu	Glu	Asp	Leu
			35				40					45			

Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80
 Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
 85 90 95
 Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
 100 105 110
 Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
 115 120 125
 Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp
 130 135 140
 Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg
 145 150 155 160
 Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln
 165 170 175
 Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp
 180 185 190
 Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val
 195 200 205
 Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
 210 215 220
 Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
 225 230 235 240
 Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
 245 250 255
 Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
 260 265 270
 Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
 275 280 285
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
 290 295 300
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
 305 310 315 320
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
 325 330 335
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
 340 345 350
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
 355 360 365
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
 370 375 380

Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn
385 390 395 400
Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
405 410 415
Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
420 425 430
Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
435 440 445
Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
450 455 460
Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
465 470 475 480
Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
485 490 495
Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
500 505 510
Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
515 520 525
Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met
530 535 540
Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu
545 550 555 560
Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His
565 570 575
Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys
580 585 590
Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe
595 600 605
Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu
610 615 620
Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser
625 630 635 640
Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu
645 650 655
Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu
660 665 670
Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser
675 680 685
Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe
690 695 700
Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr
705 710 715 720

Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
 805 810 815
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
 820 825 830
 Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu
 835 840 845
 Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr
 850 855 860
 Tyr Asp Tyr Asn Ser Asp Arg Trp
 865 870

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
 1 5 10 15
 Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn
 20 25 30
 Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
 35 40 45
 Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
 50 55 60
 Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
 65 70 75 80
 Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
 85 90 95
 Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
 100 105 110

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
450 455 460
Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys
465 470 475 480
Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile
485 490 495
Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg
500 505 510
Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys
515 520 525
Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met
530 535 540
Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg
545 550 555 560
Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
565 570 575
Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
580 585 590
Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
595 600 605
Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
610 615 620
Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile
625 630 635 640
Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
645 650 655
Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
660 665 670
Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu
675 680 685
Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
690 695 700
Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe
705 710 715 720
Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
725 730 735
Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
740 745 750
Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
755 760 765
Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
770 775 780

His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
785 790 795 800

Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
805 810 815

Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
820 825 830

Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
835 840 845

Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
850 855 860

Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
865 870 875 880

His Ile Val Asn

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

DGTDATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Cys Val Ser Tyr Ile Leu Ser Ser Phe Tyr Tyr Ala Asn Leu Glu
1 5 10 15

Glu Asn Ala Leu Gln Phe Leu Arg Lys Glu Ser Met Asp Pro Glu Lys
20 25 30

Pro Glu Thr Asn Leu Leu Met Arg Leu Thr
35 40

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu
1 5 10 15

Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn
20 25 30

Pro Asn Val Asn Leu Leu Met Arg Leu Thr
35 40

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "RNA"

(ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 12..25
(D) OTHER INFORMATION: /mod_base= OTHER
/note= "The residues located at these positions are
2-O-methylribonucleoti..."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TAGACCTGTT AGGUUUUGGG GUUUUG

26

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGGGTTTTGG GGT

16

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: /note= "expressed sequence tag (EST)
AA281296"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCAAGTTCC TGC	ACTGGCT	GATGAGTGTG	TACGTCGTCG	AGCTGCTCAG	GTCTTTCTTT	60
TATGTCACGG	AGACCACGTT	TCAAAGAAC	AGGCTCTTTT	TCTACCGGAA	GAGTGTCTGG	120
AGCAAGTTGC	AAAGCATTGG	AATCAGACAG	CAC TTGAAGA	GGGTGCAGCT	GCGGGACGTG	180
TCGGAAGCAG	AGGTCAGGCA	GCATCGGGAA	GCCAGGCCCG	CCCTGCTGAC	GTCCAGACTC	240
CGCTTCATCC	CCAAGCCTGA	CGGGCTGCGG	CCGATTGTGA	ACATGGACTA	CGTCGTGGGA	300
GCCAGAACGT	TCCGCAGAGA	AAAGAGGGCC	GAGCGTCTCA	CCTCGAGGGT	GAAGGC	360
TTCAGCGTGC	TCAACTACGA	GCGGGCGCG				389

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile	Ser	Glu	Ile	Glu	Trp	Leu	Val	Leu	Gly	Lys	Arg	Ser	Asn	Ala	Lys
1				5					10					15	
Met	Cys	Leu	Ser	Asp	Phe	Glu	Lys	Arg	Lys	Gln	Ile	Phe	Ala	Glu	Phe
				20				25					30		

Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe
35 40 45

Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe
50 55 60

Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met
65 70 75 80

Lys Met Glu Ala Phe Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp
85 90 95

Thr Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys
100 105 110

Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile
115 120 125

Lys Met Gly Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu
130 135 140

Arg Pro Val Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser
145 150 155 160

Gly Ile Pro Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys
165 170 175

Lys Asp Leu Leu Lys His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val
180 185 190

Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met
195 200 205

Phe Arg Ile Val Lys Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg
210 215 220

Lys Tyr Ala Thr Ile His Ala Thr Ser
225 230

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from *Saccharomyces cerevisiae* EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys
1 5 10 15

His Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp
 20 25 30
 Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys
 35 40 45
 Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr
 50 55 60
 Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr
 65 70 75 80
 Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser
 85 90 95
 Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
 100 105 110
 Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu
 115 120 125
 Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln
 130 135 140
 Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys
 145 150 155 160
 Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln
 165 170 175
 Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met
 180 185 190
 Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys
 195 200 205
 Met Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val
 210 215 220
 Arg Ser Gln Tyr Phe Phe Asn Thr Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser Ala Lys His Phe
 1 5 10 15
 Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp Lys Leu Leu Arg
 20 25 30
 Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
 35 40 45
 Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 50 55 60
 Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
 65 70 75 80
 Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu Trp Lys Lys
 85 90 95
 Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr
 100 105 110
 Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val Asn Ser Asp
 115 120 125
 Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu Asn Ser His
 130 135 140
 Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp Pro Phe Gly
 145 150 155 160
 Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr Glu Glu Phe
 165 170 175
 Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe Phe Ala Thr
 180 185 190
 Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg Glu Lys Leu Ser
 195 200 205
 Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp Phe Trp Ile Met
 210 215 220
 Thr Ala Gln Ile Leu Lys Arg Lys Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2631
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATTTATACTC ATGAAAATCT TATTCGAGTT CATTCAAGAC AAGCTTGACA TTGATCTACA 60
GACCAACAGT ACTTACAAAG AAAATTTAAA ATGTGGTCAC TTCAATGGCC TCGATGAAAT 120
TCTAACTACG TGTTTCGCAC TACCAAATTC AAGAAAAATA GCATTACCAT GCCTTCCTGG 180
TGACTTAAGC CACAAAGCAG TCATTGATCA CTGCATCATT TACCTGTTGA CGGGCGAATT 240
ATACAACAAC GTACTAACAT TTGGCTATAA AATAGCTAGA AATGAAGATG TCAACAATAG 300
TCTTTTTTGC CATTCTGCAA ATGTTAACGT TACGTTACTG AAAGGCGCTG CTTGGAAAAAT 360
GTTCCACAGT TTGGTCGGTA CATACGCATT CGTTGATTTA TTGATCAATT ATACAGTAAT 420
TCAATTTAAT GGGCAGTTTT TCACTCAAAT CGTGGGTAAC AGATGTAACG AACCTCATCT 480
GCCGCCCAAA TGGGTCCAAC GATCATCCTC ATCATCCGCA ACTGCTGCGC AAATCAAACA 540
ACTTACAGAA CCAGTGACAA ATAAACAATT CTTACACAAG CTCAATATAA ATTCCTCTTC 600
TTTTTTTCCT TATAGCAAGA TCCTTCCTTC ATCATCATCT ATCAAAAAGC TAACTGACTT 660
GAGAGAAGCT ATTTTCCCA CAAATTGGT TAAAATTCCT CAGAGACTAA AGGTACGAAT 720
TAATTTGACG CTGCAAAAGC TATTAAAGAG ACATAAGCGT TTGAATTACG TTTCTATTTT 780
GAATAGTATT TGCCCACCAT TGGGAAGGGAC CGTATTGGAC TTGTCGCATT TGAGTAGGCA 840
ATCACCAAAG GAACGAGTCT TGAAATTTAT CATTGTTATT TTACAGAAGT TATTACCCCA 900
AGAAATGTTT GGCTCAAAGA AAAATAAAGG AAAAATTATC AAGAATCTAA ATCTTTTATT 960
AAGTTTACCC TTAAATGGCT ATTTACCATT TGATAGTTTG TTGAAAAAGT TAAGATTAAA 1020
GGATTTTCGG TGGTGTGTC TTTCTGATAT TTGGTTCACC AAGCACAATT TTGAAAACCT 1080
GAATCAATTG GCGATTTGTT TCATTTCCTG GCTATTTAGA CAACTAATTC CAAAATTAT 1140
ACAGACTTTT TTTTACTGCA CCGAAATATC TTCTACAGTG ACAATTGTTT ACTTTAGACA 1200
TGATACTTGG AATAAACTTA TCACCCCTTT TATCGTAGAA TATTTTAAGA CGTACTTAGT 1260
CGAAAACAAC GTATGTAGAA ACCATAATAG TTACACGTTG TCCAATTTCA ATCATAGCAA 1320
AATGAGGATT ATACCAAAAA AAAGTAATAA TGAGTTCAGG ATTATTGCCA TCCCATGCAG 1380
AGGGGCAGAC GAAGAAGAAT TCACAATTTA TAAGGAGAAT CACAAAAATG CTATCCAGCC 1440
CACTCAAAAA ATTTTAGAAT ACCTAAGAAA CAAAAGGCCG ACTAGTTTTA CTAATAATATA 1500
TTCTCCAACG CAAATAGCTG ACCGTATCAA AGAATTTAAG CAGAGACTTT TAAAGAAATT 1560
TAATAATGTC TTACCAGAGC TTTATTTTAT GAAATTTGAT GTCAAATCTT GCTATGATTC 1620
CATACCAAGG ATGGAATGTA TGAGGATACT CAAGGATGCG CTAAAAAATG AAAATGGGTT 1680
TTTCGTTAGA TCTCAATATT TCTTCAATAC CAATACAGGT GTATTGAAGT TATTTAATGT 1740
TGTTAACGCT AGCAGAGTAC CAAAACCTTA TGAGCTATAC ATAGATAATG TGAGGACGGT 1800

TEATTTATCA AATCAGGATG TTATAAACGT TGTAGAGATG GAAATATTTA AAACAGCTTT	1860
GTGGGTTGAA GATAAGTGCT ACATTAGAGA AGATGGTCTT TTTCAGGGCT CTAGTTTATC	1920
TGCTCCGATC GTTGATTTGG TGTATGACGA TCTTCTGGAG TTTTATAGCG AGTTTAAAGC	1980
CAGTCCTAGC CAGGACACAT TAATTTTAAA ACTGGCTGAC GATTTCTTA TAATATCAAC	2040
AGACCAACAG CAAGTGATCA ATATCAAAAA GCTTGCCATG GCGGATTTT AAAAAATATAA	2100
TGCGAAAGCC AATAGAGACA AAATTTTAGC CGTAAGCTCC CAATCAGATG ATGATACGGT	2160
TATTCAATTT TGTGCAATGC ACATATTTGT TAAAGAATTG GAAGTTTGA AACATTCAAG	2220
CACAATGAAT AATTTCCATA TCCGTTTCGAA ATCTAGTAAA GGGATATTTT GAAGTTTAAT	2280
AGCGCTGTTT AACACTAGAA TCTCTTATAA AACAATTGAC ACAAATTTAA ATTCAACAAA	2340
CACCGTTCTC ATGCAAATTG ATCATGTTGT AAAGAACATT TCGGAATGTT ATAAATCTGC	2400
TTTTAAGGAT CTATCAATTA ATGTTACGCA AAATATGCAA TTTCATTTCGT TCTTACAACG	2460
CATCATTGAA ATGACAGTCA GCGGTTGTCC AATTACGAAA TGTGATCCTT TAATCGAGTA	2520
TGAGGTACGA TTCACCATAT TGAATGGATT TTTGGAAAGC CTATCTTCAA ACACATCAAA	2580
ATTTAAAGAT AATATCATTC TTTTGAGAAA GGAAATTCAA CACTTGCAAG C	2631

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: /note= "TRT motifs from human"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala	Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu
1				5					10					15	
Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu
			20					25					30		
Phe	Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile
			35				40					45			
Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu
			50			55					60				
Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu
65					70					75				80	

Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
85 90 95
Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
100 105 110
Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
115 120 125
Ala

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(959..1216, 1273..1353, 1425..1543, 1595..1857, 1894..2286, 2326..2396, 2436..2705, 2746..2862, 2914..3083, 3125..3309, 3356..3504, 3546..3759, 3797..4046, 4086..4252, 4296..4392, 4435..4597)
- (D) OTHER INFORMATION: /note= "Schizosaccharomyces pombe telomerase catalytic subunit (TRT) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGTACCGATT TACTTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT	60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAAGT CAAATTCCAA TATGAAGGTG	120
TTATTAGTGA TCGATAATAT TTCTATTTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG	180
AACAACTTCC TTCCCCCTAA AGACTTTTAC TTTATTAATT TACTTTTCAA ATATATTTTCG	240
GGTTCGCTTA CTTTTAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGTT	300
TCTACCCCGT CATTGGATAT AGCTCTTGGA GTAGCTCACA GAAATCCTTA CAAATCTTCT	360
GATGAGACTA TATTAGATTC ATTACAGTCC GTGCATATTC TTAACATGGA GCCTTACACT	420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTTG CCTTGAAAAG	480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGGTA ATCCGCGAAA GTTTTGTGAT	540
GCTTGACACAC GTCTAGCATG ATTGAGATAT TCAAAAATTT CTATCCACTA CAACTCCTTT	600
AACGCGGTTT TATTTTCTA TTTTCTATTC TCATGTTGTT CCAAATATGT ATCATCTCGT	660
ATTAGGCTTT TTTCCGTTTT ACTCCTGGAA TCGTACCTTT TCACTATTC CCCCTAATGA	720
ATAATCTAAA TTAGTTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG	780

TSTAATGTTA TTAGTTTAAA GATACTTTGC AAAACATTTA TTAGCTATCA TTATATAAAA 840
AAAATCCTAT AATTATAAAT ATTAATCAAT ATTTGCGGTC ACTATTTATT TAAAACGTTA 900
TGATCAGTAG GACACTTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC 958
ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG 1006
Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu
1 5 10 15
AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT 1054
Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val
20 25 30
TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG 1102
Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu
35 40 45
AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA 1150
Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val
50 55 60
GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro
65 70 75 80
AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGTTTTG ATTTTTTCT 1246
Lys Cys Ser Gln Ser Glu
85
ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG 1299
Leu Ile Ala Asn Val Val Lys Gln Met
90 95
TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT 1347
Phe Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe
100 105 110
TCC ATG GTAAGGTATT CTAATTGTGA AATATTTACC TGCAATTACT GTTTCAAAGA 1403
Ser Met
GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA 1454
Asn His Glu Asp Phe Arg Ala Met His Val
115 120
AAC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA 1502
Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile
125 130 135
TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT 1543
Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Leu Glu Ile
140 145 150
GTAAATACCG GTTAAGATGT TGCGCACTTT GAACAAGACT GACAAGTATA G T ATC 1598
Ile
GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG 1646
Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu
155 160 165 170

GCT CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT Ala Leu Pro Asn Asp Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe 175 180 185	1694
AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr 190 195 200	1742
ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser 205 210 215	1790
TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser 220 225 230	1838
TAT AAG AAG TTT AAG CAA G GTAAC TAATA CTGTTATCCT TCATAACTAA Tyr Lys Lys Phe Lys Gln 235 240	1887
TTTTAG AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr 245 250	1934
GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile 255 260 265 270	1982
AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser 275 280 285	2030
CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile 290 295 300	2078
GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr 305 310 315	2126
AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu 320 325 330	2174
AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile 335 340 345 350	2222
CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe 355 360 365	2270
GAG ATA ATA TTA AAA G GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAG AC Glu Ile Ile Leu Lys 370 Asp	2327
CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His 375 380 385	2375
TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTTTT ACCATTAATT Tyr Leu Met Ser Asn Ile Lys	2426

390

395

AACAAATCAG ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA 2474
 Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser
 400 405

AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT 2522
 Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe
 410 415 420

GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA 2570
 Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu
 425 430 435 440

CAA TCT TTT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT 2618
 Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr
 445 450 455

GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT 2666
 Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile
 460 465 470

ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTTAAA 2715
 Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu
 475 480 485

GTATTTTTTG CAAAAAGCTA ATATTTTCAG AAC AAT GTT AGG ATG GAT ACT CAG 2769
 Asn Asn Val Arg Met Asp Thr Gln
 490

AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT 2817
 Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn
 495 500 505

ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG 2862
 Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys
 510 515 520

GTATTAATTT TTGGTCATCA ATGTACTTTA CTTCTAATCT ATTATTAGCA G ATG GGT 2919
 Met Gly
 525

TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967
 Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val
 530 535 540

GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA 3015
 Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro
 545 550 555

TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT 3063
 Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu
 560 565 570

CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT 3113
 Leu Lys His Arg Met Phe Gly
 575 580

TAATTTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC 3161
 Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser
 585 590

TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG 3209
 Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys
 595 600 605

AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT 3257
 Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His
 610 615 620 625

GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC 3305
 Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser
 630 635 640

TAT T GTAAGTTTAT TTTTTCATTG GAATTTTSTA ACAAATTCTT TTTTAG TT 3357
 Tyr Phe

GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA 3405
 Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr
 645 650 655

TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT 3453
 Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser
 660 665 670 675

TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT 3501
 Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val
 680 685 690

AAG GTATACCAAT TGTGGAATTG TAATAACACT AATGAAACTA G ATA GGA AAT 3554
 Lys Ile Gly Asn
 695

TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA 3602
 Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser
 700 705 710

TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA 3650
 Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu
 715 720 725

TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT 3698
 Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp
 730 735 740

TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT 3746
 Phe Leu Phe Ile Thr Val Asn Lys Lys Asp Ala Lys Lys Phe Leu Asn
 745 750 755

TTA TCT TTA AGA G GTGAGTTGCT GTCATTCCTA AGTTCTAACC GTTGAAG GA 3798
 Leu Ser Leu Arg Gly

TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC 3846
 Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn
 765 770 775 780

TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC 3894
 Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser
 785 790 795

AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT 3942
 Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu

	800	805	810	
GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT				3990
Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser	815	820	825	
ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA				4038
Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys	830	835	840	
ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG				4089
Ile Leu Arg Ser	845			
AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA				4137
Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser	850	855	860	
AAA TTC AAT TCT TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT				4185
Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys	865	870	875 880	
ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC				4233
Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro	885	890	895	
CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTTAACTA GAAAAGTCAT				4282
Gln Arg Met Phe Ile Thr	900			
TAATTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA				4330
Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys	905	910		
AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT				4378
Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser	915	920	925 930	
GCA GAA GTC AAA TG GTACGTGTCG GTCTCGAGAC TTCAGCAATA TTGACACATC				4432
Ala Glu Val Lys Trp	935			
AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA				4480
Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys	940	945	950	
TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT				4528
Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr	955	960	965	
GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA				4576
Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu	970	975	980	
CAT AGA AGA ATA GCT GAT TAATGTCATT TTCAATTTAT TATATACATC				4624
His Arg Arg Ile Ala Asp	985			
CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC				4684
ATACTATAGG ATTTCTAGTA AAGTAAATT AATCTCGTTA TTAGTTTTGA TTGACTTGTC				4744

TTTATCCTTA TACTTTTAAG AAAGATTGAC AGTGGTTGCT GACTACTGCC CACATGCCCCA	4804
TTAAACGGGA GTGGTTAAAC ATTAAAGTA ATACATGAGG CTAATCTCCT TTCATTTAGA	4864
ATAAGGAAAG TGGTTTTCTA TAATGAATAA TGCCCGCACT AATGCAAAAA GACGAAGATT	4924
ATCTTCTAAA CAAGGGGGAT TAAGCATATC CGAAGGAAAA GAGAGTAATA TACCCAGTGT	4984
TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTTGG	5044
TGACCGAATT TTGGTAAAAG CCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACG	5104
AAAAGAACT AAGGATAGTT TGAATACTAA TAGCTCATTT AATGTCTTAT ATAAGGTTTT	5164
GTTTTTTCCT GACTTCAATT TTGCATGGGT GAAAAGAAAT AGTGTTAAGC CATTATTGGA	5224
TTCCGAAATA GCCAAATTTC TTGGTTCCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC	5284
TTATGAGGCT TCAAAAACCTC CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT	5344
GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTTG CAAAAAGAA AATATCATTG	5404
GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT	5464
AACTTCTATT TCTGAAATGT ATGGTCCTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA	5524
GTTAAGTGAC CAAAGGTACC	5544

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu	
1 5 10 15	
Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val	
20 25 30	
Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu	
35 40 45	
Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val	
50 55 60	
Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro	
65 70 75 80	
Lys Cys Ser Gln Ser Glu Leu Ile Ala Asn Val Val Lys Gln Met Phe	
85 90 95	
Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe Ser	
100 105 110	
Met Asn His Glu Asp Phe Arg Ala Met His Val Asn Gly Val Gln Asn	

115					120					125					
Asp	Leu	Val	Ser	Thr	Phe	Pro	Asn	Tyr	Leu	Ile	Ser	Ile	Leu	Glu	Ser
130						135					140				
Lys	Asn	Trp	Gln	Leu	Leu	Leu	Glu	Ile	Ile	Gly	Ser	Asp	Ala	Met	His
145					150					155					160
Tyr	Leu	Leu	Ser	Lys	Gly	Ser	Ile	Phe	Glu	Ala	Leu	Pro	Asn	Asp	Asn
				165					170					175	
Tyr	Leu	Gln	Ile	Ser	Gly	Ile	Pro	Leu	Phe	Lys	Asn	Asn	Val	Phe	Glu
		180					185						190		
Glu	Thr	Val	Ser	Lys	Lys	Arg	Lys	Arg	Thr	Ile	Glu	Thr	Ser	Ile	Thr
		195					200					205			
Gln	Asn	Lys	Ser	Ala	Arg	Lys	Glu	Val	Ser	Trp	Asn	Ser	Ile	Ser	Ile
	210					215					220				
Ser	Arg	Phe	Ser	Ile	Phe	Tyr	Arg	Ser	Ser	Tyr	Lys	Lys	Phe	Lys	Gln
225					230					235					240
Asp	Leu	Tyr	Phe	Asn	Leu	His	Ser	Ile	Cys	Asp	Arg	Asn	Thr	Val	His
				245					250					255	
Met	Trp	Leu	Gln	Trp	Ile	Phe	Pro	Arg	Gln	Phe	Gly	Leu	Ile	Asn	Ala
		260					265						270		
Phe	Gln	Val	Lys	Gln	Leu	His	Lys	Val	Ile	Pro	Leu	Val	Ser	Gln	Ser
	275						280					285			
Thr	Val	Val	Pro	Lys	Arg	Leu	Leu	Lys	Val	Tyr	Pro	Leu	Ile	Glu	Gln
	290					295					300				
Thr	Ala	Lys	Arg	Leu	His	Arg	Ile	Ser	Leu	Ser	Lys	Val	Tyr	Asn	His
305					310					315					320
Tyr	Cys	Pro	Tyr	Ile	Asp	Thr	His	Asp	Asp	Glu	Lys	Ile	Leu	Ser	Tyr
				325					330					335	
Ser	Leu	Lys	Pro	Asn	Gln	Val	Phe	Ala	Phe	Leu	Arg	Ser	Ile	Leu	Val
			340					345					350		
Arg	Val	Phe	Pro	Lys	Leu	Ile	Trp	Gly	Asn	Gln	Arg	Ile	Phe	Glu	Ile
		355					360					365			
Ile	Leu	Lys	Asp	Leu	Glu	Thr	Phe	Leu	Lys	Leu	Ser	Arg	Tyr	Glu	Ser
	370					375					380				
Phe	Ser	Leu	His	Tyr	Leu	Met	Ser	Asn	Ile	Lys	Ile	Ser	Glu	Ile	Glu
385					390					395					400
Trp	Leu	Val	Leu	Gly	Lys	Arg	Ser	Asn	Ala	Lys	Met	Cys	Leu	Ser	Asp
				405					410					415	
Phe	Glu	Lys	Arg	Lys	Gln	Ile	Phe	Ala	Glu	Phe	Ile	Tyr	Trp	Leu	Tyr
			420				425						430		
Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr	Ile	Thr	Glu
		435					440						445		

Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys Asp Ile Trp
 450 455 460
 Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met Glu Ala Phe
 465 470 475 480
 Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr
 485 490 495
 Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg
 500 505 510
 Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn
 515 520 525
 Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val Ala Ser
 530 535 540
 Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro Phe Asn
 545 550 555 560
 Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu Leu Lys
 565 570 575
 His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys
 580 585 590
 Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
 595 600 605
 Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile
 610 615 620
 His Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe
 625 630 635 640
 Ser Tyr Phe Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser
 645 650 655
 Met Lys Thr Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr
 660 665 670
 Lys Ser Ser Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly
 675 680 685
 His Ile Val Lys Ile Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile
 690 695 700
 Pro Gln Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
 705 710 715 720
 Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val
 725 730 735
 Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
 740 745 750
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
 755 760 765
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn Ser
 770 775 780

Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser Lys Lys Arg Met
 785 790 795 800
 Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu Asp Thr Leu Leu
 805 810 815
 Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser Thr Ser Val Glu
 820 825 830
 Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys Ile Leu Arg Ser
 835 840 845
 Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser
 850 855 860
 Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys
 865 870 875 880
 Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro
 885 890 895
 Gln Arg Met Phe Ile Thr Asp Leu Leu Asn Val Ile Gly Arg Lys Ile
 900 905 910
 Trp Lys Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu
 915 920 925
 Ser Ser Ala Glu Val Lys Trp Leu Phe Cys Leu Gly Met Arg Asp Gly
 930 935 940
 Leu Lys Pro Ser Phe Lys Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr
 945 950 955 960
 Gln Phe Gln Ser Leu Thr Asp Leu Ile Lys Pro Leu Arg Pro Val Leu
 965 970 975
 Arg Gln Val Leu Phe Leu His Arg Arg Ile Ala Asp
 980 985

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = guanosine modified by a biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

NCCTATTTYT TYTAYNNNAC NGA

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Phe Phe Tyr Xaa Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asp Asp Phe Leu Xaa Ile
1 5

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACAATGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2..3

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Arg Xaa Xaa Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACGAATCKNG GDATNSWRTC RTARCA

26

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Cys Tyr Asp Ser Ile Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asp Ile Lys Ser Cys Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATTACTCCC GAAGAAAGGA TCTTTCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC 60
AAAAAATAT TAAGTTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACTT GTGTTTAGGA 120
ATTTAAAAGA CATGCTGGGA TAAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATTT 180
CAGAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAAATAA AGGAAGACCT CAGCTATATT 240
ATGTCACTCT AGACATAAAG ACTTGCTAC 269

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAACACAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT	60
AAATTAAC TAAGTCAAGT AAGAATTTAG TTTTCTGAAA AGAATAAATA AATGAAAAAT	120
AATTTTTATC AAAAAATTTA GCTTGAAGAG GAGAATTTGG AAAAAGTTGA AGAAAAATTG	180
ATACCAGAAG ATTCATTTTA GAAATACCTT CAAGGAAAGC TAAGGATTAT ACCTAAAAAA	240
GGATCTTTCC GTCCAATCAT GACTTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA	300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTTA GGAATTTAAA AGACATGCTG	360
GGATAAAGA TAGGATACTC AGTCTTTGAT AATAAACAAA TTTCAGAAAA ATTTGCCTAA	420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA	474

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Lys	His	Lys	Glu	Gly	Ser	Gln	Ile	Phe	Tyr	Tyr	Arg	Lys	Pro	Ile	Trp
1				5					10					15	
Lys	Leu	Val	Ser	Lys	Leu	Thr	Ile	Val	Lys	Val	Arg	Ile	Gln	Phe	Ser
			20					25					30		
Glu	Lys	Asn	Lys	Gln	Met	Lys	Asn	Asn	Phe	Tyr	Gln	Lys	Ile	Gln	Leu
		35					40					45			
Glu	Glu	Glu	Asn	Leu	Glu	Lys	Val	Glu	Glu	Lys	Leu	Ile	Pro	Glu	Asp
		50				55					60				
Ser	Phe	Gln	Lys	Tyr	Pro	Gln	Gly	Lys	Leu	Arg	Ile	Ile	Pro	Lys	Lys
65					70					75				80	
Gly	Ser	Phe	Arg	Pro	Ile	Met	Thr	Phe	Leu	Arg	Lys	Asp	Lys	Gln	Lys
				85					90					95	
Asn	Ile	Lys	Leu	Asn	Leu	Asn	Gln	Ile	Leu	Met	Asp	Ser	Gln	Leu	Val
			100				105						110		
Phe	Arg	Asn	Leu	Lys	Asp	Met	Leu	Gly	Gln	Lys	Ile	Gly	Tyr	Ser	Val
		115					120					125			
Phe	Asp	Asn	Lys	Gln	Ile	Ser	Glu	Lys	Phe	Ala	Gln	Phe	Ile	Glu	Lys

130

135

140

Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu
 145 150 155

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Phe Tyr Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe
 1 5 10 15
 Arg His Asp Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr
 20 25 30
 Phe Lys Thr Tyr Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser
 35 40 45
 Tyr Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys
 50 55 60
 Lys Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala
 65 70 75 80
 Asp Glu Glu Glu Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile
 85 90 95
 Gln Pro Thr Gln Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr
 100 105 110
 Ser Phe Thr Lys Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys
 115 120 125
 Glu Phe Lys Gln Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu
 130 135 140
 Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr
 1 5 10 15
 Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp
 20 25 30
 Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu
 35 40 45
 Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro
 50 55 60
 Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val
 65 70 75 80
 Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu
 85 90 95
 Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp
 100 105 110
 Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr
 115 120 125
 Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe
 130 135 140
 Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys His Lys Glu Gly Ser Gln Ile Phe Tyr Tyr Arg Lys Pro Ile Trp
 1 5 10 15
 Lys Leu Val Ser Lys Leu Thr Ile Val Lys Val Arg Ile Gln Phe Ser
 20 25 30
 Glu Lys Asn Lys Gln Met Lys Asn Asn Phe Tyr Gln Lys Ile Gln Leu
 35 40 45
 Glu Glu Glu Asn Leu Glu Lys Val Glu Glu Lys Leu Ile Pro Glu Asp
 50 55 60
 Ser Phe Gln Lys Tyr Pro Gln Gly Lys Leu Arg Ile Ile Pro Lys Lys
 65 70 75 80
 Gly Ser Phe Arg Pro Ile Met Thr Phe Leu Arg Lys Asp Lys Gln Lys
 85 90 95

Asn Ile Lys Leu Asn Leu Asn Gln Ile Leu Met Asp Ser Gln Leu Val
100 105 110

Phe Arg Asn Leu Lys Asp Met Leu Gly Gln Lys Ile Gly Tyr Ser Val
115 120 125

Phe Asp Asn Lys Gln Ile Ser Glu Lys Phe Ala Gln Phe Ile Glu Lys
130 135 140

Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala
1 5 10 15

Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp
20 25 30

Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys
35 40 45

Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr
50 55 60

Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu
65 70 75 80

Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val
85 90 95

Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys
100 105 110

Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu
115 120 125

Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn
130 135 140

Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr
145 150 155 160

Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe
165 170 175

Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp
180 185 190

Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys
 195 200 205
 Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn
 210 215 220
 Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile
 225 230 235 240
 Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His
 245 250 255
 Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln
 260 265 270
 Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu
 275 280 285
 Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys
 290 295 300
 Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu
 305 310 315 320
 Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr
 325 330 335
 Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr
 340 345 350
 Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile
 355 360 365
 Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys
 370 375 380
 Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys
 385 390 395 400
 Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln
 405 410 415
 Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile
 420 425 430
 Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val
 435 440 445
 Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr
 450 455 460
 Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys
 465 470 475 480
 Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu
 485 490 495
 Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
 500 505 510
 Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
 515 520 525

Asn	Lys	Lys	Ile	Val	Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr	
530						535						540				
Asn	Thr	Lys	Leu	Leu	Asn	Ser	His	Leu	Met	Leu	Lys	Thr	Leu	Lys	Asn	
545					550					555					560	
Arg	Met	Phe	Lys	Asp	Pro	Phe	Gly	Phe	Ala	Val	Phe	Asn	Tyr	Asp	Asp	
				565					570					575		
Val	Met	Lys	Lys	Tyr	Glu	Glu	Phe	Val	Cys	Lys	Trp	Lys	Gln	Val	Gly	
			580					585					590			
Gln	Pro	Lys	Leu	Phe	Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp	
		595					600					605				
Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys	Thr	Thr	Lys	Leu	
	610					615					620					
Leu	Ser	Ser	Asp	Phe	Trp	Ile	Met	Thr	Ala	Gln	Ile	Leu	Lys	Arg	Lys	
625					630					635					640	
Asn	Asn	Ile	Val	Ile	Asp	Ser	Lys	Asn	Phe	Arg	Lys	Lys	Glu	Met	Lys	
				645					650					655		
Asp	Tyr	Phe	Arg	Gln	Lys	Phe	Gln	Lys	Ile	Ala	Leu	Glu	Gly	Gly	Gln	
			660					665					670			
Tyr	Pro	Thr	Leu	Phe	Ser	Val	Leu	Glu	Asn	Glu	Gln	Asn	Asp	Leu	Asn	
		675					680					685				
Ala	Lys	Lys	Thr	Leu	Ile	Val	Glu	Ala	Lys	Gln	Arg	Asn	Tyr	Phe	Lys	
	690					695					700					
Lys	Asp	Asn	Leu	Leu	Gln	Pro	Val	Ile	Asn	Ile	Cys	Gln	Tyr	Asn	Tyr	
705					710					715					720	
Ile	Asn	Phe	Asn	Gly	Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro	Gln	
				725					730					735		
Gly	Leu	Cys	Val	Ser	Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr	Leu	
			740					745					750			
Glu	Glu	Ser	Ser	Leu	Gly	Phe	Leu	Arg	Asp	Glu	Ser	Met	Asn	Pro	Glu	
		755					760					765				
Asn	Pro	Asn	Val	Asn	Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	Leu	
	770					775					780					
Ile	Thr	Thr	Gln	Glu	Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	Ile	
785					790					795					800	
Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln	
				805					810					815		
Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lys	Phe	Ala	Lys	Tyr	Gly	Met	Asp	
			820					825					830			
Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile	Gly	
		835					840					845				
Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala								

Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys
865 870 875 880

Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn
885 890 895

Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala
900 905 910

Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met
915 920 925

Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met
930 935 940

Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr
945 950 955 960

Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe
965 970 975

Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe
980 985 990

Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
995 1000 1005

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCAC TGTTTCAGCG

19

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGATGATT TCTTGTGG

19

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGCAGGAGG ATCTTGTAG

19

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGACCCCAGG AGTGGCAGG

19

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCAAGCTGAC TCGACACCG

19

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGGCGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTGAAGGCT GAGTGTCC

18

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 22..1716
 (D) OTHER INFORMATION: /note= "EcoRI-NotI insert of
 clone 712562 encoding 63 kDa

telomerase protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCAAGTTCC TGC	ACTGGCT GATGAGTGTG	TACGTCGTCG AGCTGCTCAG	GTCTTTCTTT	60
TATGTCACGG AGA	CCAGTT TCAAAAGAAC	AGGCTCTTTT TCTACCGGAA	GAGTGTCTGG	120
AGCAAGTTGC AA	AGCATTGG AATCAGACAG	CACCTGAAGA GGGTGCAGCT	GCGGGAGCTG	180
TCGGAAGCAG AG	GTCAGGCA GCATCGGGAA	GCCAGGCCCG CCCTGCTGAC	GTCCAGACTC	240
CGCTTCATCC C	CAAGCCTGA CGGGCTGCGG	CCGATTGTGA ACATGGACTA	CGTCGTGGGA	300
GCCAGAACGT T	CCGCAGAGA AAAGARGGCC	GAGCGTCTCA CCTCGAGGGT	GAAGGCACTG	360
TTCAGCGTGC T	CAACTACGA GCGGGCGCGG	CGCCCCGGCC TCCTGGGCGC	CTCTGTGCTG	420
GGCCTGGACG A	TATCCACAG GGCCTGGCGC	ACCTTCGTGC TGC	GTGTGCG GGGCCAGGAC	480
CCGCCGCCTG A	GCTGTACTT TGTCAAGGTG	GATGTGACGG GCGCGTACGA	CACCATCCCC	540
CAGGACAGGC T	CACGGAGGT CATCGCCAGC	ATCATCAAAC CCCAGAACAC	GTACTGCGTG	600
CGTCGGTATG C	CGTGGTCCA GAAGGCCGCC	ATGGGCACGT CCGCAAGGCC	TTCAAGAGCC	660
ACGTCCTACG T	CCAGTGCCA GGGGATCCCC	CAGGGCTCCA TCCTCTCCAC	GCTGCTCTGC	720
AGCCTGTGCT A	CGGCGACAT GGAGAACAAG	CTGTTTGCGG GGATTTCGGCG	GGACGGGCTG	780
CTCCTGCGTT T	GGTGGATGA TTTCTTGTTG	GTGACACCTC ACCTCACCCA	CGCGAAAACC	840
TTCTCAGGA C	CTGGTCCG AGGTGTCCCT	GAGTATGGCT GCGTGGTGAA	CTTGCGGAAG	900
ACAGTGGTGA A	CTTCCCTGT AGAAGACGAG	GCCCTGGGTG GCACGGCTTT	TGTTCAAGATG	960
CCGGCCCACG G	CCTATTCCC CTGGTGCGGC	CTGCTGCTGG ATACCCGGAC	CCTGGAGGTG	1020
CAGAGCGACT A	CTCCAGCTA TGCCCGGACC	TCCATCAGAG CCAGTCTCAC	CTTCAACCGC	1080
GGCTTCAAGG C	TGGGAGGAA CATGCGTCGC	AAACTCTTTG GGGTCTTGCG	GCTGAAGTGT	1140
CACAGCCTGT T	CTTGATTT GCAGGTGAAC	AGCCTCCAGA CGGTGTGCAC	CAACATCTAC	1200
AAGATCCTCC T	GCTGCAGGC GTACAGGTTT	CACGCATGTG TGCTGCAGCT	CCCATTTCAT	1260
CAGCAAGTTT G	GGAAGAACC ACATTTTTC	TGCGCGTCAT CTCTGACACG	GCTCCCTCTG	1320
CTACTCCATC C	TGAAAGCCA AGAACGCAGG	GATGTCGCTG GGGGCCAAGG	GCGCCGCCGG	1380
CCCTCTGCCC T	CCGAGGCCG TGCAGTGGCT	GTGCCACCAA GCATTCCTGC	TCAAGCTGAC	1440
TCGACACCGT G	TACCTACG TGCCACTCCT	GGGGTCACTC AGGACAGCCC	AGACGCAGCT	1500
GAGTCGGAAG C	TCCCGGGGA CGACGCTGAC	TGCCCTGGAG GCCGCAGCCA	ACCCGGCACT	1560
GCCCTCAGAC T	TCAAGACCA TCCTGGACTG	ATGGCCACCC GCCCACAGCC	AGGCCGAGAG	1620
CAGACACCAG C	AGCCCTGTC ACGCCGGGCT	TATACGTCCC AGGGAGGGAG	GGGCGGCCCA	1680
CACCCAGGCC T	GCACCGCTG GGAGTCTGAG	GCCTGAGTGA GTGTTTGGCC	GAGGCCTGCA	1740

TGTCCGGCTG AAGGCTGAGT GTCCGGCTGA GGCCTGAGCG AGTGTCCAGC CAAGGGCTGA 1800
 GTGTCCAGCA CACCTGCGTT TTCACCTCCC CACAGGCTGG CGTTCGGTCC ACCCCAGGGC 1860
 CAGCTTTTCC TCACCAGGAG CCCGGCTTCC ACTCCCCACA TAGGAATAGT CCATCCCCAG 1920
 ATTCCGCATT GTTCACCCTT CGCCCTGCCT TCCTTTGCCT TCCACCCCCA CCATTCCAGT 1980
 GGAGACCCTG AGAAGGACCC TGGGAGCTTT GGGAAATTGG AGTGACCAA GGTGTGCCCT 2040
 GTACACAGGC GAGGACCCTG CACCTGGATG GGGGTCCCTG TGGGTCAAAT TGGGGGGAGG 2100
 TGCTGTGGGA GTAAATACT GAATATATGA GTTTTTCAGT TTTGGAAAAA AAAAAAAAAA 2160
 AAAAAAAAAA A 2171

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..564
- (D) OTHER INFORMATION: /note= "63 kDa telomerase protein encoded by ORF of EcoRI-NotI insert of clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr
 1 5 10 15
 Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val
 20 25 30
 Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val
 35 40 45
 Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala
 50 55 60
 Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp
 65 70 75 80
 Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr
 85 90 95
 Phe Arg Arg Glu Lys Xaa Ala Glu Arg Leu Thr Ser Arg Val Lys Ala
 100 105 110
 Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu
 115 120 125

Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr
 130 135 140
 Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe
 145 150 155 160
 Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg
 165 170 175
 Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys
 180 185 190
 Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala Met Gly Thr Ser Ala
 195 200 205
 Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
 210 215 220
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
 225 230 235 240
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
 245 250 255
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
 260 265 270
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 275 280 285
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 290 295 300
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 305 310 315 320
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 325 330 335
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 340 345 350
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 355 360 365
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 370 375 380
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 385 390 395 400
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 405 410 415
 Trp Lys Asn Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg Leu Pro
 420 425 430
 Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp Val Ala Gly Gly
 435 440 445
 Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg Ala Val Ala Val
 450 455 460

Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro Cys His Leu Arg
 465 470 475 480

Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala Ala Glu Ser Glu
 485 490 495

Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg Ser Gln Pro Gly
 500 505 510

Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met Ala Thr Arg Pro
 515 520 525

Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser Arg Arg Ala Tyr
 530 535 540

Thr Ser Gln Gly Gly Arg Gly Gly Pro His Pro Gly Leu His Arg Trp
 545 550 555 560

Glu Ser Glu Ala

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTTT TTTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCAGTGAGCA GAGTGACG

18

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAGGACTCGA GCTCAAGC

18

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CACTGATCCT TTCTTTTTCG TAAACGATAG GT

32

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATCAATCAA ATCTTCCATA TAGAAATGAC A

31

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 5'-phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

NGGCCGTGTT GGCCTAGTTC TCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCCCC

38

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGTCATTTC TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACCTATCGTT TACGAAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAGTGACATA ATATACGTGA

20

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe
1 5 10 15
Tyr Arg Lys Ser Val Trp Ser Lys
20

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu
1 5 10 15
Val Arg Gln His Arg Glu Ala
20

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
1 5 10 15
Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
20 25

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
1 5 10 15

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln
20 25

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
1 5 10 15

Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly
1 5 10 15

Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
20 25

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Gln Thr Lys Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

NGTNATDARD ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Asp Asp Tyr Leu Leu Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe
1 5 10 15
Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu
20 25 30
Ser Met Asn Pro Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr
35 40 45
Asp Asp Tyr Leu Leu Ile Thr
50 55

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile
1 5 10 15
Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg
20 25 30
Val Val

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile Val Asp Leu
1 5 10 15
Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys Ala Ser Pro
20 25 30
Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
35 40 45
Ser

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gln Lys Val Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CAAAAAGTTG GTATCCCTCA GGG

23

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AGACCAAAGG AATTCCATCA GGCTCAATTC TGTCATCTTT TTTGTGTCAT TTCTATATGG

60

AAGATTTGAT TGATGAATAC CTATCGTTTA CGAAAAAGAA AGGATCAGTG TTGTTACGAG

120

TAGTCGACGA CTACCTCCTC ATCACC

146

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Gly Ile Pro Ser Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe
1 5 10 15
Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys
 20 25 30
Gly Ser Val Leu Leu Arg Val Val Asp Asp Tyr Leu Leu Ile Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GACGATTTCC TCTTTATAAC A

21

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Asp Phe Leu Phe Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

AAAAAAAAAA AAAAAA

16

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TTTTTTTTTT TTTTTT

17

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif 0 peptide from Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Trp	Leu	Tyr	Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr
1				5				10						15	
Ile	Thr	Glu	Ser	Ser	Asp	Leu	Arg	Asn	Arg	Thr	Val	Tyr	Phe	Arg	Lys
			20					25					30		
Asp	Ile	Trp													
		35													

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys	Asn	Thr	Phe	Arg	Leu	Ile	Thr
1				5					10					15	

Asn Leu Arg Lys Arg Phe
20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /note= "motif 3(A) peptide from
Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile
1 5 10 15

Lys Gln Asp Leu Met Phe Arg Ile Val Lys
20 25

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..32
(D) OTHER INFORMATION: /note= "motif 4(B') peptide from
Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe
1 5 10 15

Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Schizosaccharomyces pombe tezip"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys
1 5 10 15

Lys Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys
20 25 30

His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn
35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif 0 peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
1 5 10 15

Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
20 25 30

Thr Trp

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu Phe Arg Ile
1 5 10 15
Ile Ala Ile Pro Cys Arg Gly Ala Asp
 20 25

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 3(A) peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile
1 5 10 15
Pro Arg Met Glu Cys Met Arg Ile Leu Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide

- (B) LOCATION: 1..32
 (D) OTHER INFORMATION: /note= "motif 4(B') peptide from
 Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro
 1 5 10 15
 Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe
 20 25 30

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..49
 (D) OTHER INFORMATION: /note= "motif 5(C) peptide from
 Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln
 1 5 10 15
 Gln Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys
 20 25 30
 Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala Val Ser Ser Gln
 35 40 45
 Ser

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
 (B) LOCATION: 1..35
 (D) OTHER INFORMATION: /note= "motif 0 peptide from
 Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1 5 10 15
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
20 25 30
Asn Ile Trp
35

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met
1 5 10 15
Thr Phe Asn Lys Lys Ile Val
20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 3(A) peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val
1 5 10 15

Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 4(B') peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile
1 5 10 15
Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu
1 5 10 15
Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu
20 25 30
Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro Leu
35 40 45
Ser

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln
1 5 10 15
Lys Ser Tyr Ser Lys Thr
 20

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "motif 0 peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys
1 5 10 15
Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val
 20 25 30

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif A peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser
1 5 10 15

Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif B peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys
1 5 10 15

Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala
20 25

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 22

(D) OTHER INFORMATION: /note= "motif C peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile
1 5 10 15

Thr Thr Gln Glu Asn Asn
20

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser
1 5 10 15

Asp Leu Arg Asn Arg Thr
20

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..30
 - (D) OTHER INFORMATION: /note= "motif 0 peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Gln	Lys	Thr	Thr	Leu	Pro	Pro	Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys
1				5					10					15	
Asn	Thr	Phe	Arg	Leu	Ile	Thr	Asn	Leu	Arg	Lys	Arg	Phe	Leu		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..27
 - (D) OTHER INFORMATION: /note= "motif A peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Arg	Lys	Lys	Tyr	Phe	Val	Arg	Ile	Asp	Ile	Lys	Ser	Cys	Tyr	Asp	Arg
1				5				10						15	
Ile	Lys	Gln	Asp	Leu	Met	Phe	Arg	Ile	Val	Lys					
			20					25							

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile
1 5 10 15
Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile
1 5 10 15
Thr Val Asn Lys Lys Asp
 20

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His Asn Phe Ser Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..22
 - (D) OTHER INFORMATION: /note= "motif 1 peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr Glu Ile Ser
 1 5 10 15
 Ser Thr Val Thr Ile Val
 20

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..32
 - (D) OTHER INFORMATION: /note= "motif 0 peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys
 1 5 10 15
 Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser
1 5 10 15
Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Glu Asp Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser
1 5 10 15
Leu Ser Ala Pro Ile Val Asp Leu Val Tyr Asp
 20 25

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide

(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "motif C peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
1 5 10 15
Ser Thr Asp Gln Gln Gln
20

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide.
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /note= "motif D peptide from
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide.
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /note= "motif 1 peptide from human
telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
1 5 10 15
Phe Gln Lys Asn Arg Leu
20

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "motif 0 peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro
1 5 10 15
Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
 20 25 30

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr
1 5 10 15
Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif B peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile
1 5 10 15

Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly
20 25

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..22

(D) OTHER INFORMATION: /note= "motif C peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val
1 5 10 15

Thr Pro His Leu Thr His
20

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..15

(D) OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Phe Phe Tyr Val Thr Glu
1 5

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4029 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY:
(B) LOCATION: 1..4029
(D) OTHER INFORMATION: /note= "preliminary sequence for
human TRT cDNA insert of
plasmid pGRN121"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCGATGCC	60
GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC AGCCACTACC GCGAGGTGCT	120
GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG	180
GGACCCGGCG GCTTTCCGCG CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN	240
ANGGCNGCCC CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC	300
CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT TCGGCTTCGC	360
GCTGCTGGAC GGGGCCCCGCG GGGGCCCCCC CGAGGCCTTC ACCACCAGCG TGCGCAGCTA	420
CCTGCCCAAC ACGGTGACCG ACGCACTGCG GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG	480
CCGCGTGGGC GACGACGTGC TGGTTCACCT GCTGGCACGC TGCGCGNTNT TTGTGCTGGT	540

GGNTCCCAGC	TGCGCCTACC	ANGTGTGCGG	GCCGCCGCTG	TACCAGCTCG	GCGCTGCNAC	600
TCAGGCCCCG	CCCCCGCCAC	ACGCTANTGG	ACCCGAANGC	GTCTGGGATC	CAACGGGCCT	660
GGAACCATAG	CGTCAGGGAG	GCCGGGGTCC	CCCTGGGCTG	CCAGCCCCGG	GTGCGAGGAG	720
GCGCGGGGGC	AGTGCCAGCC	GAAGTCTGCC	GTTGCCCAAG	AGGCCCAGGC	GTGGCGCTGC	780
CCCTGAGCCG	GAGCGGACGC	CCGTTGGGCA	GGGGTCCTGG	GCCCACCCGG	GCAGGACGCC	840
TGGACCGAGT	GACCGTGGTT	TCTGTGTGGT	GTCACCTGCC	AGACCCGCCG	AAGAAGCCAC	900
CTCTTTGGAG	GGTGCCTCT	CTGGCACGCG	CCACTCCCAC	CCATCCGTGG	GCCGCCAGCA	960
CCACGCGGGC	CCCCCATCCA	CATCGCGGCC	ACCACGTCCT	GGGACACGCC	TTGTCCCCCG	1020
GTGTACGCCG	AGACCAAGCA	CTTCCTCTAC	TCCTCAGGCG	ACAAGNACAC	TGCGNCCCTC	1080
CTTCCTACTC	AATATATCTG	AGGCCCAGCC	TGACTGGCGT	TCGGGAGGTT	CGTGGAGACA	1140
NTCTTTCTGG	TTCCAGGCCT	TGGATGCCAG	GATTCCCCGC	AGGTTGCCCC	GCCTGCCCCA	1200
GCGNTACTGG	CAAATGCGGC	CCCTGTTTCT	GGAGCTGCTT	GGGAACCACG	CGCAGTGCCC	1260
CTACGGGGTG	TTCTCAAGA	CGCACTGCCC	GCTGCGAGCT	GCGGTCAACC	CAGCAGCCGG	1320
TGTCTGTGCC	CGGGAGAAGC	CCCAGGGCTC	TGTGGCGGCC	CCCGAGGAGG	AGGAACACAG	1380
ACCCCCGTCG	CCTGGTGCAG	CTGCTCCGCC	AGCACAGCAG	CCCCTGGCAG	GTGTACGGCT	1440
TCGTGCGGGC	CTGCCTGCGC	CGGCTGGTGC	CCCCAGGCCT	CTGGGGCTCC	AGGCACAACG	1500
AACGCCGCTT	CCTCAGGAAC	ACCAAGAAGT	TCATCTCCCT	GGGGAAGCAT	GCCAAGCTCT	1560
CGCTGCAGGA	GCTGACGTGG	AAGATGAGCG	TGCGGGACTG	CGCTTGGCTG	CGCAGGAGCC	1620
CAGGGGTTGG	CTGTGTTCCG	GCCGCAGAGC	ACCGTCTGCG	TGAGGAGATC	CTGGCCAAGT	1680
TCCTGCACTG	GCTGATGAGT	GTGTACGTCG	TCGAGCTGCT	CAGGTCTTTC	TTTTATGTCA	1740
CGGAGACCAC	GTTTCAAAAG	AACAGGCTCT	TTTTCTACCG	GAAGAGTGTC	TGGAGCAAGT	1800
TGCAAAGCAT	TGGAATCAGA	CAGCACTTGA	AGAGGGTGCA	GCTGCGGGAG	CTGTCCGAAG	1860
CAGAGGTCAG	GCAGCATCGG	GAAGCCAGGC	CCGCCCTGCT	GACGTCCAGA	CTCCGCTTCA	1920
TCCCCAAGCC	TGACGGGCTG	CGGCCGATTG	TGAACATGGA	CTACGTCTGT	GGAGCCAGAA	1980
CGTTCCGCAG	AGAAAAGAGG	GCCGAGCGTC	TCACCTCGAG	GGTGAAGGCA	CTGTTCAAGC	2040
TGCTCAACTA	CGAGCGGGCG	CGGCGCCCCG	GCCTCCTGGG	CGCCTCTGTG	CTGGGCCTGG	2100
ACGATATCCA	CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	GCGGGCCCAG	GACCCGCCGC	2160
CTGAGCTGTA	CTTTGTCAAG	GTGGATGTGA	CGGGCGCGTA	CGACACCATC	CCCCAGGACA	2220
GGCTCACGGA	GGTCATCGCC	AGCATCATCA	AACCCAGAA	CACGTACTGC	GTGCGTCGGT	2280
ATGCCGTGGT	CCAGAAGGCC	GCCCATGGGC	ACGTCCGCAA	GGCCTTCAAG	AGCCACGTCT	2340
CTACCTTGAC	AGACCTCCAG	CCGTACATGC	GACAGTTCGT	GGCTCACCTG	CAGGANAACA	2400

GCCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG GCCAGCAGTG	2460
GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC CGTGCGCATC AGGGGCAAGT	2520
CCTACGTCCA GTGCCAGGGG ATCCCGCAGG GCTCCATCCT CTCCACGCTG CTCTGCAGCC	2580
TGTGCTACGG CGACATGGAG AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC	2640
TGCGTTTGGT GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC	2700
TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG CGGAAGACAG	2760
TGGTGAACCT CCCTGTAGAA GACGAGGCC TGGGTGGCAC GGCTTTTGTT CAGATGCCGG	2820
CCCACGGCCT ATTCCCCTGG TCGGGCCTGC TGCTGGATAC CCGGACCCTG GAGGTGCAGA	2880
GCGACTACTC CAGCTATGCC CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT	2940
TCAAGGCTGG GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCACA	3000
GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC ATCTACAAGA	3060
TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT GCAGCTCCCA TTTCATCAGC	3120
AAGTTTGGA GAACCCACA TTTTTCCTGC GCGTCATCTC TGACACGGCC TCCCTCTGCT	3180
ACTCCATCCT GAAAGCCAAG AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC	3240
CTCTGCCCTC CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCTGCTC AAGCTGACTC	3300
GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG ACGCAGCTGA	3360
GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC CGCAGCCAAC CCGGCACTGC	3420
CCTCAGACTT CAAGACCATC CTGGACTGAT GGCCACCCGC CCACAGCCAG GCCGAGAGCA	3480
GACACCAGCA GCCCTGTCAC GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC	3540
CCAGGCCCCG ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT	3600
CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA GGGCTGAGTG	3660
TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG CTCGGCTCCA CCCCAGGGCC	3720
AGCTTTTCCT CACCAGGAGC CCGGCTTCCA CTCCCCACAT AGGAATAGTC CATCCCCAGA	3780
TTCGCCATTG TTCACCCCTC GCCCTGCCCT CTTTGCCTT CCACCCCCAC CATCCAGGTG	3840
GAGACCCCTGA GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG	3900
TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT GGGGGGAGGT	3960
GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT TTGAAAAAA AAAAAAAA	4020
AAAAAAA	4029

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ala Ala Leu Arg Pro Ala Ala His Val Gly Ser Pro Gly Pro Gly His
1 5 10 15
Pro Arg Asp Ala Ala Arg Ser Pro Leu Pro Ser Arg Ala Leu Pro Ala
20 25 30
Ala Gln Pro Leu Pro Arg Gly Ala Ala Gly His Val Arg Ala Ala
35 40 45
Pro Gly Ala Pro Gly Leu Ala Ala Gly Ala Ala Arg Gly Pro Gly Gly
50 55 60
Phe Pro Arg Xaa Gly Gly Pro Xaa Xaa Gly Val Arg Ala Leu Gly Xaa
65 70 75 80
Xaa Ala Ala Pro Arg Arg Pro Leu Leu Pro Pro Gly Val Leu Pro Glu
85 90 95
Xaa Xaa Gly Gly Pro Ser Ala Ala Xaa Ala Val Arg Xaa Arg Arg Glu
100 105 110
Xaa Arg Ala Gly Leu Arg Leu Arg Ala Ala Gly Arg Gly Pro Arg Gly
115 120 125
Pro Pro Arg Gly Leu His His Gln Arg Ala Gln Leu Pro Ala Gln His
130 135 140
Gly Asp Arg Arg Thr Ala Gly Glu Arg Gly Val Gly Ala Ala Ala Ala
145 150 155 160
Pro Arg Gly Arg Arg Arg Ala Gly Ser Pro Ala Gly Thr Leu Arg Xaa
165 170 175
Xaa Cys Ala Gly Gly Ser Gln Leu Arg Leu Pro Xaa Val Arg Ala Ala
180 185 190
Ala Val Pro Ala Arg Arg Cys Xaa Ser Gly Pro Ala Pro Ala Thr Arg
195 200 205
Xaa Trp Thr Arg Xaa Arg Leu Gly Ser Asn Gly Pro Gly Thr Ile Ala
210 215 220
Ser Gly Arg Pro Gly Ser Pro Trp Ala Ala Ser Pro Gly Cys Glu Glu
225 230 235 240
Ala Arg Gly Gln Cys Gln Pro Lys Ser Ala Val Ala Gln Glu Ala Gln
245 250 255
Ala Trp Arg Cys Pro
260

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Ala Gly Ala Asp Ala Arg Trp Ala Gly Val Leu Gly Pro Pro Gly Gln
 1 5 10 15
 Asp Ala Trp Thr Glu
 20

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Pro Trp Phe Leu Cys Gly Val Thr Cys Gln Thr Arg Arg Arg Ser His
 1 5 10 15
 Leu Phe Gly Gly Cys Ala Leu Trp His Ala Pro Leu Pro Pro Ile Arg
 20 25 30
 Gly Pro Pro Ala Pro Arg Gly Pro Pro Ile His Ile Ala Ala Thr Thr
 35 40 45
 Ser Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe
 50 55 60
 Leu Tyr Ser Ser Gly Asp Lys Xaa Thr Ala Xaa Leu Leu Pro Thr Gln
 65 70 75 80
 Tyr Ile

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Leu Ala Phe Gly Arg Phe Val Glu Thr Xaa Phe Leu Val Pro Gly Leu
 1 5 10 15
 Gly Cys Gln Asp Ser Pro Gln Val Ala Pro Pro Ala Pro Ala Xaa Leu
 20 25 30
 Ala Asn Ala Ala Pro Val Ser Gly Ala Ala Trp Glu Pro Arg Ala Val
 35 40 45
 Pro Leu Arg Gly Val Pro Gln Asp Ala Leu Pro Ala Ala Ser Cys Gly
 50 55 60
 His Pro Ser Ser Arg Cys Leu Cys Pro Gly Glu Ala Pro Gly Leu Cys
 65 70 75 80
 Gly Gly Pro Arg Gly Gly Gly Thr Gln Thr Pro Val Ala Trp Cys Ser
 85 90 95
 Cys Ser Ala Ser Thr Ala Ala Pro Gly Arg Cys Thr Ala Ser Cys Gly
 100 105 110
 Pro Ala Cys Ala Gly Trp Cys Pro Gln Ala Ser Gly Ala Pro Gly Thr
 115 120 125
 Thr Asn Ala Ala Ser Ser Gly Thr Pro Arg Ser Ser Ser Pro Trp Gly
 130 135 140
 Ser Met Pro Ser Ser Arg Cys Arg Ser
 145 150

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Ala Cys Gly Thr Ala Leu Gly Cys Ala Gly Ala Gln Gly Leu Ala Val
 1 5 10 15
 Phe Arg Pro Gln Ser Thr Val Cys Val Arg Arg Ser Trp Pro Ser Ser
 20 25 30
 Cys Thr Gly
 35

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Val Cys Thr Ser Ser Ser Cys Ser Gly Leu Ser Phe Met Ser Arg Arg
1 5 10 15
Pro Arg Phe Lys Arg Thr Gly Ser Phe Ser Thr Gly Arg Val Ser Gly
20 25 30
Ala Ser Cys Lys Ala Leu Glu Ser Asp Ser Thr
35 40

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Arg Gly Cys Ser Cys Gly Ser Cys Arg Lys Gln Arg Ser Gly Ser Ile
1 5 10 15
Gly Lys Pro Gly Pro Pro Cys
20

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Arg Pro Asp Ser Ala Ser Ser Pro Ser Leu Thr Gly Cys Gly Arg Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Thr Trp Thr Thr Ser Trp Glu Pro Glu Arg Ser Ala Glu Lys Arg Gly
1 5 10 15
Pro Ser Val Ser Pro Arg Gly
20

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Arg His Cys Ser Ala Cys Ser Thr Thr Ser Gly Arg Gly Ala Pro Ala
1 5 10 15
Ser Trp Ala Pro Leu Cys Trp Ala Trp Thr Ile Ser Thr Gly Pro Gly
20 25 30
Ala Pro Ser Cys Cys Val Cys Gly Pro Arg Thr Arg Arg Leu Ser Cys
35 40 45
Thr Leu Ser Arg Trp Met
50

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Arg Ala Arg Thr Thr Pro Ser Pro Arg Thr Gly Ser Arg Arg Ser Ser
1 5 10 15
Pro Ala Ser Ser Asn Pro Arg Thr Arg Thr Ala Cys Val Gly Met Pro
20 25 30
Trp Ser Arg Arg Pro Pro Met Gly Thr Ser Ala Arg Pro Ser Arg Ala
35 40 45
Thr Ser Leu Pro
50

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Gln Thr Ser Ser Arg Thr Cys Asp Ser Ser Trp Leu Thr Cys Arg Xaa
 1 5 10 15
 Thr Ala Arg

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Gly Met Pro Ser Ser Ser Ser Arg Ala Pro Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Arg Pro Ala Val Ala Ser Ser Thr Ser Ser Tyr Ala Ser Cys Ala
 1 5 10 15
 Thr Thr Pro Cys Ala Ser Gly Ala Ser Pro Thr Ser Ser Ala Arg Gly
 20 25 30
 Ser Arg Arg Ala Pro Ser Ser Pro Arg Cys Ser Ala Ala Cys Ala Thr
 35 40 45
 Ala Thr Trp Arg Thr Ser Cys Leu Arg Gly Phe Gly Gly Thr Gly Cys
 50 55 60
 Ser Cys Val Trp Trp Met Ile Ser Cys Trp
 65 70

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

His Leu Thr Ser Pro Thr Arg Lys Pro Ser Ser Gly Pro Trp Ser Glu
1 5 10 15

Val Ser Leu Ser Met Ala Ala Trp
 20

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Thr Cys Gly Arg Gln Trp
1 5

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Thr Arg Pro Trp Val Ala Arg Leu Leu Phe Arg Cys Arg Pro Thr
1 5 10 15

Ala Tyr Ser Pro Gly Ala Ala Cys Cys Trp Ile Pro Gly Pro Trp Arg
 20 25 30

Cys Arg Ala Thr Thr Pro Ala Met Pro Gly Pro Pro Ser Glu Pro Val
 35 40 45

Ser Pro Ser Thr Ala Ala Ser Arg Leu Gly Gly Thr Cys Val Ala Asn
 50 55 60

Ser Leu Gly Ser Cys Gly
65 70

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Ser Val Thr Ala Cys Phe Trp Ile Cys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Thr Ala Ser Arg Arg Cys Ala Pro Thr Ser Thr Arg Ser Ser Cys Cys
1 5 10 15
Arg Arg Thr Gly Phe Thr His Val Cys Cys Ser Ser His Phe Ile Ser
20 25 30
Lys Phe Gly Arg Thr Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg
35 40 45
Pro Pro Ser Ala Thr Pro Ser
50 55

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Lys Pro Arg Thr Gln Gly Cys Arg Trp Gly Pro Arg Ala Pro Pro Ala
1 5 10 15

Leu Cys Pro Pro Arg Pro Cys Ser Gly Cys Ala Thr Lys His Ser Cys
 20 25 30

Ser Ser

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Leu Asp Thr Val Ser Pro Thr Cys His Ser Trp Gly His Ser Gly Gln
 1 5 10 15

Pro Arg Arg Ser
 20

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Val Gly Ser Ser Arg Gly Arg Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Pro Trp Arg Pro Gln Pro Thr Arg His Cys Pro Gln Thr Ser Arg
 1 5 10 15

Pro Ser Trp Thr Asp Gly His Pro Pro Thr Ala Arg Pro Arg Ala Asp
 20 25 30

Thr Ser Ser Pro Val Thr Pro Gly Ser Thr Ser Gln Gly Gly Arg Gly
 35 40 45

Gly Pro His Pro Gly Pro His Arg Trp Glu Ser Glu Ala
 50 55 60

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Val Ser Val Trp Pro Arg Pro Ala Cys Pro Ala Glu Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Gly Leu Ser Glu Cys Pro Ala Lys Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Val Ser Ser Thr Pro Ala Val Phe Thr Ser Pro Gln Ala Gly Ala Arg
 1 5 10 15

Leu His Pro Arg Ala Ser Phe Ser Ser Pro Gly Ala Arg Leu Pro Leu
 20 25 30

Pro Thr

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Ser Ile Pro Arg Phe Ala Ile Val His Pro Ser Pro Cys Pro Pro Leu
1 5 10 15
Pro Ser Thr Pro Thr Ile Gln Val Glu Thr Leu Arg Arg Thr Leu Gly
20 25 30
Ala Leu Gly Ile Trp Ser Asp Gln Arg Cys Ala Leu Tyr Thr Gly Glu
35 40 45
Asp Pro Ala Pro Gly Trp Gly Ser Leu Trp Val Lys Leu Gly Gly Gly
50 55 60
Ala Val Gly Val Lys Tyr
65 70

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Ile Tyr Glu Phe Phe Ser Phe Glu Lys Lys Lys Lys Lys Lys Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala Thr
1 5 10 15

Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu
 20 25 30
 Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg
 35 40 45
 Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala
 50 55 60
 Phe Arg Ala Xaa Val Ala Xaa Cys Xaa Val Cys Val Pro Trp Xaa Xaa
 65 70 75 80
 Xaa Xaa Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Xaa
 85 90 95
 Xaa Leu Val Ala Arg Val Leu Xaa Xaa Leu Cys Xaa Arg Gly Ala Xaa
 100 105 110
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
 115 120 125
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
 130 135 140
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
 145 150 155 160
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Xaa
 165 170 175
 Phe Val Leu Val Xaa Pro Ser Cys Ala Tyr Xaa Val Cys Gly Pro Pro
 180 185 190
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
 195 200 205
 Xaa Gly Pro Glu Xaa Val Trp Asp Pro Thr Gly Leu Glu Pro
 210 215 220

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Arg Gln Gly Gly Arg Gly Pro Pro Gly Leu Pro Ala Pro Gly Ala Arg
 1 5 10 15
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
 20 25 30
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
 35 40 45

Ser Trp Ala His Pro Gly Arg Thr Pro Gly Pro Ser Asp Arg Gly Phe
 50 55 60
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
 65 70 75 80
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
 85 90 95
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Gly Thr
 100 105 110
 Arg Leu Val Pro Arg Cys Thr Pro Arg Pro Ser Thr Ser Ser Thr Pro
 115 120 125
 Gln Ala Thr Xaa Thr Leu Arg Pro Ser Phe Leu Leu Asn Ile Ser Glu
 130 135 140
 Ala Gln Pro Asp Trp Arg Ser Gly Gly Ser Trp Arg Xaa Ser Phe Trp
 145 150 155 160
 Phe Gln Ala Leu Asp Ala Arg Ile Pro Arg Arg Leu Pro Arg Leu Pro
 165 170 175
 Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn
 180 185 190
 His Ala Gln Cys Pro Tyr Gly Val Phe Leu Lys Thr His Cys Pro Leu
 195 200 205
 Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro
 210 215 220
 Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Glu His Arg Pro Pro Ser
 225 230 235 240
 Pro Gly Ala Ala Ala Pro Pro Ala Gln Gln Pro Leu Ala Gly Val Arg
 245 250 255
 Leu Arg Ala Gly Leu Pro Ala Pro Ala Gly Ala Pro Arg Pro Leu Gly
 260 265 270
 Leu Gln Ala Gln Arg Thr Pro Leu Pro Gln Glu His Gln Glu Val His
 275 280 285
 Leu Pro Gly Glu Ala Cys Gln Ala Leu Ala Ala Gly Ala Asp Val Glu
 290 295 300
 Asp Glu Arg Ala Gly Leu Arg Leu Ala Ala Gln Glu Pro Arg Gly Trp
 305 310 315 320
 Leu Cys Ser Gly Arg Arg Ala Pro Ser Ala
 325 330

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly Asp Pro Gly Gln Val Pro Ala Leu Ala Asp Glu Cys Val Arg Arg
1 5 10 15
Arg Ala Ala Gln Val Phe Leu Leu Cys His Gly Asp His Val Ser Lys
20 25 30
Glu Gln Ala Leu Phe Leu Pro Glu Glu Cys Leu Glu Gln Val Ala Lys
35 40 45
His Trp Asn Gln Thr Ala Leu Glu Glu Gly Ala Ala Ala Gly Ala Val
50 55 60
Gly Ser Arg Gly Gln Ala Ala Ser Gly Ser Gln Ala Arg Pro Ala Asp
65 70 75 80
Val Gln Thr Pro Leu His Pro Gln Ala
85

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Arg Ala Ala Ala Asp Cys Glu His Gly Leu Arg Arg Gly Ser Gln Asn
1 5 10 15
Val Pro Gln Arg Lys Glu Gly Arg Ala Ser His Leu Glu Gly Glu Gly
20 25 30
Thr Val Gln Arg Ala Gln Leu Arg Ala Gly Ala Ala Pro Arg Pro Pro
35 40 45
Gly Arg Leu Cys Ala Gly Pro Gly Arg Tyr Pro Gln Gly Leu Ala His
50 55 60
Leu Arg Ala Ala Cys Ala Gly Pro Gly Pro Ala Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Ala Val Leu Cys Gln Gly Gly Cys Asp Gly Arg Val Arg His His Pro
1 5 10 15
Pro Gly Gln Ala His Gly Gly His Arg Gln His His Gln Thr Pro Glu
20 25 30
His Val Leu Arg Ala Ser Val Cys Arg Gly Pro Glu Gly Arg Pro Trp
35 40 45
Ala Arg Pro Gln Gly Leu Gln Glu Pro Arg Leu Tyr Leu Asp Arg Pro
50 55 60
Pro Ala Val His Ala Thr Val Arg Gly Ser Pro Ala Gly Xaa Gln Pro
65 70 75 80
Ala Glu Gly Cys Arg Arg His Arg Ala Glu Leu Leu Pro Glu
85 90

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Gly Gln Gln Trp Pro Leu Arg Arg Leu Pro Thr Leu His Val Pro Pro
1 5 10 15
Arg Arg Ala His Gln Gly Gln Val Leu Arg Pro Val Pro Gly Asp Pro
20 25 30
Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
35 40 45
His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
50 55 60
Ala Phe Gly Gly
65

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Phe Leu Val Gly Asp Thr Ser Pro His Pro Arg Glu Asn Leu Pro Gln
 1 5 10 15
 Asp Pro Gly Pro Arg Cys Pro
 20

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Val Trp Leu Arg Gly Glu Leu Ala Glu Asp Ser Gly Glu Leu Pro Cys
 1 5 10 15
 Arg Arg Arg Gly Pro Gly Trp His Gly Phe Cys Ser Asp Ala Gly Pro
 20 25 30
 Arg Pro Ile Pro Leu Val Arg Pro Ala Ala Gly Tyr Pro Asp Pro Gly
 35 40 45
 Gly Ala Glu Arg Leu Leu Gln Leu Cys Pro Asp Leu His Gln Ser Gln
 50 55 60
 Ser His Leu Gln Pro Arg Leu Gln Gly Trp Glu Glu His Ala Ser Gln
 65 70 75 80
 Thr Leu Trp Gly Leu Ala Ala Glu Val Ser Gln Pro Val Ser Gly Phe
 85 90 95
 Ala Gly Glu Gln Pro Pro Asp Gly Val His Gln His Leu Gln Asp Pro
 100 105 110
 Pro Ala Ala Gly Val Gln Val Ser Arg Met Cys Ala Ala Ala Pro Ile
 115 120 125
 Ser Ser Ala Ser Leu Glu Glu Pro His Ile Phe Pro Ala Arg His Leu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

His Gly Leu Pro Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp

1	5	10	15												
Val	Ala	Gly	Gly	Gln	Gly	Arg	Arg	Arg	Pro	Ser	Ala	Leu	Arg	Gly	Arg
		20						25					30		
Ala	Val	Ala	Val	Pro	Pro	Ser	Ile	Pro	Ala	Gln	Ala	Asp	Ser	Thr	Pro
		35					40					45			
Cys	His	Leu	Arg	Ala	Thr	Pro	Gly	Val	Thr	Gln	Asp	Ser	Pro	Asp	Ala
	50					55					60				
Ala	Glu	Ser	Glu	Ala	Pro	Gly	Asp	Asp	Ala	Asp	Cys	Pro	Gly	Gly	Arg
65					70					75					80
Ser	Gln	Pro	Gly	Thr	Ala	Leu	Arg	Leu	Gln	Asp	His	Pro	Gly	Leu	Met
				85					90					95	
Ala	Thr	Arg	Pro	Gln	Pro	Gly	Arg	Glu	Gln	Thr	Pro	Ala	Ala	Leu	Ser
			100					105						110	
Arg	Arg	Ala	Leu	Arg	Pro	Arg	Glu	Gly	Gly	Ala	Ala	His	Thr	Gln	Ala
		115					120					125			
Arg	Thr	Ala	Gly	Ser	Leu	Arg	Pro	Glu							
		130				135									

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Val	Phe	Gly	Arg	Gly	Leu	His	Val	Arg	Leu	Lys	Ala	Glu	Cys	Pro	Ala
1				5				10					15		
Glu Ala															

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ala	Ser	Val	Gln	Pro	Arg	Ala	Glu	Cys	Pro	Ala	His	Leu	Pro	Ser	Ser
1				5				10					15		

Leu Pro His Arg Leu Ala Leu Gly Ser Thr Pro Gly Pro Ala Phe Pro
 20 25 30
 His Gln Glu Pro Gly Phe His Ser Pro His Arg Asn Ser Pro Ser Pro
 35 40 45
 Asp Ser Pro Leu Phe Thr Pro Arg Pro Ala Leu Leu Cys Leu Pro Pro
 50 55 60
 Pro Pro Ser Arg Trp Arg Pro
 65 70

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Glu Gly Pro Trp Glu Leu Trp Glu Phe Gly Val Thr Lys Gly Val Pro
 1 5 10 15
 Cys Thr Gln Ala Arg Thr Leu His Leu Asp Gly Gly Pro Cys Gly Ser
 20 25 30
 Asn Trp Gly Glu Val Leu Trp Glu
 35 40

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Asn Thr Glu Tyr Met Ser Phe Ser Val Leu Lys Lys Lys Lys Lys Lys
 1 5 10 15
 Lys Lys

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Ser Ala Ala Ser Cys Cys Ala Arg Gly Lys Pro Trp Pro Arg Pro Pro
1 5 10 15
Pro Arg Cys Arg Ala Leu Pro Ala Ala Glu Pro Cys Ala Pro Cys Cys
20 25 30
Ala Ala Thr Thr Ala Arg Cys Cys Arg Trp Pro Arg Ser Cys Gly Ala
35 40 45
Trp Gly Pro Arg Ala Gly Gly Trp Cys Ser Ala Gly Thr Arg Arg Leu
50 55 60
Ser Ala Arg Trp Trp Pro Xaa Ala Trp Cys Ala Cys Pro Gly Xaa Xaa
65 70 75 80
Gly Xaa Pro Pro Pro Pro Pro Ser Ala Arg Cys Pro Ala
85 90

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Xaa Xaa Trp Trp Pro Glu Cys Cys Xaa Xaa Cys Ala Xaa Ala Ala Arg
1 5 10 15
Xaa Thr Cys Trp Pro Ser Ala Ser Arg Cys Trp Thr Gly Pro Ala Gly
20 25 30
Ala Pro Pro Arg Pro Ser Pro Pro Ala Cys Ala Ala Thr Cys Pro Thr
35 40 45
Arg

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Pro Thr His Cys Gly Gly Ala Gly Arg Gly Gly Cys Cys Cys Ala Ala
 1 5 10 15
 Trp Ala Thr Thr Cys Trp Phe Thr Cys Trp His Ala Ala Arg Xaa Leu
 20 25 30
 Cys Trp Trp Xaa Pro Ala Ala Pro Thr Xaa Cys Ala Gly Arg Arg Cys
 35 40 45
 Thr Ser Ser Ala Leu Xaa Leu Arg Pro Gly Pro Arg His Thr Leu Xaa
 50 55 60
 Asp Pro Xaa Ala Ser Gly Ile Gln Arg Ala Trp Asn His Ser Val Arg
 65 70 75 80
 Glu Ala Gly Val Pro Leu Gly Cys Gln Pro Arg Val Arg Gly Gly Ala
 85 90 95
 Gly Ala Val Pro Ala Glu Val Cys Arg Cys Pro Arg Gly Pro Gly Val
 100 105 110
 Ala Leu Pro Leu Ser Arg Ser Gly Arg Pro Leu Gly Arg Gly Pro Gly
 115 120 125
 Pro Thr Arg Ala Gly Arg Leu Asp Arg Val Thr Val Val Ser Val Trp
 130 135 140
 Cys His Leu Pro Asp Pro Pro Lys Lys Pro Pro Leu Trp Arg Val Arg
 145 150 155 160
 Ser Leu Ala Arg Ala Thr Pro Thr His Pro Trp Ala Ala Ser Thr Thr
 165 170 175
 Arg Ala Pro His Pro His Arg Gly His His Val Leu Gly His Ala Leu
 180 185 190
 Ser Pro Gly Val Arg Arg Asp Gln Ala Leu Pro Leu Leu Leu Arg Arg
 195 200 205
 Gln Xaa His Cys Xaa Pro Pro Ser Tyr Ser Ile Tyr Leu Arg Pro Ser
 210 215 220
 Leu Thr Gly Val Arg Glu Val Arg Gly Asp Xaa Leu Ser Gly Ser Arg
 225 230 235 240
 Pro Trp Met Pro Gly Phe Pro Ala Gly Cys Pro Ala Cys Pro Ser Xaa
 245 250 255
 Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr Arg
 260 265 270
 Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu Leu
 275 280 285
 Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg Ala
 290 295 300
 Leu Trp Arg Pro Pro Arg Arg Asn Thr Asp Pro Arg Arg Leu Val
 305 310 315 320
 Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
 325 330 335

Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
 340 345 350
 His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
 355 360 365
 Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
 370 375 380
 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val
 385 390 395 400
 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
 405 410 415
 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
 420 425 430
 Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
 435 440 445
 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
 450 455 460
 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
 465 470 475 480
 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
 485 490 495
 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
 500 505 510
 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
 515 520 525
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
 530 535 540
 Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
 545 550 555 560
 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
 565 570 575
 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
 580 585 590
 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
 595 600 605
 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
 610 615 620
 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu
 625 630 635 640
 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Xaa Asn Ser Pro
 645 650 655
 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
 660 665 670

Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
 675 680 685
 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
 690 695 700
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
 705 710 715 720
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
 725 730 735
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
 740 745 750
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 755 760 765
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 770 775 780
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 785 790 795 800
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 805 810 815
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 820 825 830
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 835 840 845
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 850 855 860
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 865 870 875 880
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 885 890 895
 Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser
 900 905 910
 Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly
 915 920 925
 Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu
 930 935 940
 Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr
 945 950 955 960
 Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg
 965 970 975
 Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro
 980 985 990
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 995 1000

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Trp Pro Pro Ala His Ser Gln Ala Glu Ser Arg His Gln Gln Pro Cys
1 5 10 15
His Ala Gly Leu Tyr Val Pro Gly Arg Glu Gly Arg Pro Thr Pro Arg
20 25 30
Pro Ala Pro Leu Gly Val
35

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Gly Leu Ser Glu Cys Leu Ala Glu Ala Cys Met Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Arg Leu Ser Val Arg Leu Arg Pro Glu Arg Val Ser Ser Gln Gly Leu
1 5 10 15
Ser Val Gln His Thr Cys Arg Leu His Phe Pro Thr Gly Trp Arg Ser
20 25 30
Ala Pro Pro Gln Gly Gln Leu Phe Leu Thr Arg Ser Pro Ala Ser Thr
35 40 45

Pro His Ile Gly Ile Val His Pro Gln Ile Arg His Cys Ser Pro Leu
50 55 60

Ala Leu Pro Ser Phe Ala Phe His Pro His His Pro Gly Gly Asp Pro
65 70 75 80

Glu Lys Asp Pro Gly Ser Ser Gly Asn Leu Glu
85 90

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Pro Lys Val Cys Pro Val His Arg Arg Gly Pro Cys Thr Trp Met Gly
1 5 10 15

Val Pro Val Gly Gln Ile Gly Gly Arg Cys Cys Gly Ser Lys Ile Leu
20 25 30

Asn Ile

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Val Phe Gln Phe
1

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Lys Lys Lys Lys Lys Lys Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..3454
- (D) OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCG ATG	58
Met	
1	
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC	106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His	
5 10 15	
TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC	154
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro	
20 25 30	
CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG	202
Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala	
35 40 45	
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC	250
Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro	
50 55 60 65	
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG	298
Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val	
70 75 80	
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG	346
Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu	
85 90 95	
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG	394
Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu	
100 105 110	
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC	442
Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp	
115 120 125	

GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly 130 135 140 145	490
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu 150 155 160	538
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln 165 170 175	586
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro 180 185 190	634
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu 195 200 205	682
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGC Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly 210 215 220 225	730
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874
TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu 275 280 285	922
TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala 290 295 300 305	970
GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys 310 315 320	1018
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp 325 330 335	1066
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser 340 345 350	1114
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg 355 360 365	1162
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg	1210

370					375					380					385	
TAC	TGG	CAA	ATG	CGG	CCC	CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	1258
Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	
				390					395					400		
CAG	TGC	CCC	TAC	GGG	GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	1306
Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	
			405					410						415		
GCG	GTC	ACC	CCA	GCA	GCC	GGT	GTC	TGT	GCC	CGG	GAG	AAG	CCC	CAG	GGC	1354
Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	
			420				425						430			
TCT	GTG	GCG	GCC	CCC	GAG	GAG	GAG	GAC	ACA	GAC	CCC	CGT	CGC	CTG	GTG	1402
Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	
			435				440					445				
CAG	CTG	CTC	CGC	CAG	CAC	AGC	AGC	CCC	TGG	CAG	GTG	TAC	GGC	TTC	GTG	1450
Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	
			450			455				460					465	
CGG	GCC	TGC	CTG	CGC	CGG	CTG	GTG	CCC	CCA	GGC	CTC	TGG	GGC	TCC	AGG	1498
Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	
				470					475					480		
CAC	AAC	GAA	CGC	CGC	TTC	CTC	AGG	AAC	ACC	AAG	AAG	TTC	ATC	TCC	CTG	1546
His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	
			485					490					495			
GGG	AAG	CAT	GCC	AAG	CTC	TCG	CTG	CAG	GAG	CTG	ACG	TGG	AAG	ATG	AGC	1594
Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	
			500				505					510				
GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT	GGC	TGT	GTT	1642
Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
			515			520						525				
CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG	GCC	AAG	TTC	CTG	1690
Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
					535					540					545	
CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	AGG	TCT	TTC	TTT	1738
His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
				550					555					560		
TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	CTC	TTT	TTC	TAC	CGG	1786
Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	
				565				570					575			
AAG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	GGA	ATC	AGA	CAG	CAC	TTG	1834
Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	
				580			585					590				
AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	GAA	GCA	GAG	GTC	AGG	CAG	CAT	1882
Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	
						600					605					
CGG	GAA	GCC	AGG	CCC	GCC	CTG	CTG	ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	1930
Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	
					615					620					625	

AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314
CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu 755 760 765	2362
CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro 770 775 780 785	2410
CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala 790 795 800	2458
AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala 805 810 815	2506
GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln 820 825 830	2554
GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met 835 840 845	2602
GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg 850 855 860 865	2650
TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys	2698

870										875										880										
ACC	TTC	CTC	AGG	ACC	CTG	GTC	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG															2746
Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val															
			885						890																					
GTG	AAC	TTG	CGG	AAG	ACA	GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC															2794
Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala															
		900						905						910																
CTG	GGT	GGC	ACG	GCT	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC	CCC															2842
Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro															
	915					920						925																		
TGG	TGC	GGC	CTG	CTG	CTG	GAT	ACC	CGG	ACC	CTG	GAG	GTG	CAG	AGC	GAC															2890
Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp															
930						935						940			945															
TAC	TCC	AGC	TAT	GCC	CGG	ACC	TCC	ATC	AGA	GCC	AGT	CTC	ACC	TTC	AAC															2938
Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr	Phe	Asn															
				950					955					960																
CGC	GGC	TTC	AAG	GCT	GGG	AGG	AAC	ATG	CGT	CGC	AAA	CTC	TTT	GGG	GTC															2986
Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val															
			965					970					975																	
TTG	CGG	CTG	AAG	TGT	CAC	AGC	CTG	TTT	CTG	GAT	TTG	CAG	GTG	AAC	AGC															3034
Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	Ser															
		980					985						990																	
CTC	CAG	ACG	GTG	TGC	ACC	AAC	ATC	TAC	AAG	ATC	CTC	CTG	CTG	CAG	GCG															3082
Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile	Leu	Leu	Leu	Gln	Ala															
	995					1000						1005																		
TAC	AGG	TTT	CAC	GCA	TGT	GTG	CTG	CAG	CTC	CCA	TTT	CAT	CAG	CAA	GTT															3130
Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro	Phe	His	Gln	Gln	Val															
1010					1015					1020				1025																
TGG	AAG	AAC	CCC	ACA	TTT	TTC	CTG	CGC	GTC	ATC	TCT	GAC	ACG	GCC	TCC															3178
Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	Val	Ile	Ser	Asp	Thr	Ala	Ser															
				1030					1035					1040																
CTC	TGC	TAC	TCC	ATC	CTG	AAA	GCC	AAG	AAC	GCA	GGG	ATG	TCG	CTG	GGG															3226
Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	Asn	Ala	Gly	Met	Ser	Leu	Gly															
			1045					1050					1055																	
GCC	AAG	GGC	GCC	GCC	GGC	CCT	CTG	CCC	TCC	GAG	GCC	GTG	CAG	TGG	CTG															3274
Ala	Lys	Gly	Ala	Ala	Gly	Pro	Leu	Pro	Ser	Glu	Ala	Val	Gln	Trp	Leu															
		1060					1065					1070																		
TGC	CAC	CAA	GCA	TTC	CTG	CTC	AAG	CTG	ACT	CGA	CAC	CGT	GTC	ACC	TAC															3322
Cys	His	Gln	Ala	Phe	Leu	Leu	Lys	Leu	Thr	Arg	His	Arg	Val	Thr	Tyr															
	1075					1080					1085																			
GTG	CCA	CTC	CTG	GGG	TCA	CTC	AGG	ACA	GCC	CAG	ACG	CAG	CTG	AGT	CGG															3370
Val	Pro	Leu	Leu	Gly	Ser	Leu	Arg	Thr	Ala	Gln	Thr	Gln	Leu	Ser	Arg															
1090					1095					1100				1105																
AAG	CTC	CCG	GGG	ACG	ACG	CTG	ACT	GCC	CTG	GAG	GCC	GCA	GCC	AAC	CCG															3418
Lys	Leu	Pro	Gly	Thr	Thr	Leu	Thr	Ala	Leu	Glu	Ala	Ala	Ala	Asn	Pro															
				1110					1115					1120																

GEA CTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CCGCCACAG 3471
Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1125 1130

CCAGGCCGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA 3531

GGGGCGGCCC ACACCCAGGC CCGCACCGCT GGGAGTCTGA GGCCTGAGTG AGTGTTTGGC 3591

CGAGGCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCCAG 3651

CCAAGGGCTG AGTGTCCAGC ACACCTGCCG TCTTCAC TTC CCCACAGGCT GGCCTCGGC 3711

TCCACCCCAG GGCCAGCTTT TCCTCACCAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT 3771

AGTCCATCCC CAGATTCGCC ATTGTTTACC CCTCGCCCTG CCCTCCTTTG CCTTCCACCC 3831

CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC 3891

AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGGTCC CTGTGGGTCA 3951

AATTGGGGGG AGGTGCTGTG GGAGTAAAT ACTGAATATA TGAGTTTTTC AGTTTTGAAA 4011

AAAA 4015

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480

Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	
				485					490					495		
Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	
			500					505					510			
Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	
		515					520					525				
Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	
	530					535					540					
Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	
545					550					555					560	
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	
			565					570						575		
Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	
			580					585					590			
Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	
		595					600					605				
His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	
	610					615					620					
Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	
625					630					635					640	
Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	
			645						650					655		
Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	
			660					665					670			
Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	
		675					680					685				
Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	
	690					695					700					
Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	
705					710					715					720	
Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	
			725						730					735		
Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	
			740					745					750			
Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp	
		755					760					765				
Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser	
	770					775					780					
Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu	
785					790					795				800		
Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	His	
			805					810						815		

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
1045 1050 1055

Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
1060 1065 1070

Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
1075 1080 1085

Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
1090 1095 1100

Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1125 1130